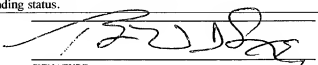


JC03 Rec'd PCT/PTO 27 APR 2001

FORM PTO-1390 (Modified) (REV 5-93)		U.S. DEPARTMENT OF COMMERCE PATENT AND TRADEMARK OFFICE		ATTORNEY'S DOCKET NUMBER	
TRANSMITTAL LETTER TO THE UNITED STATES DESIGNATED/ELECTED OFFICE (DO/EO/US) CONCERNING A FILING UNDER 35 U.S.C. 371				032931/0251	
INTERNATIONAL APPLICATION NO. PCT/CA99/00992		INTERNATIONAL FILING DATE 28 October 1999		U.S. APPLICATION NO. (If known) PCT/CA99/00992 To be assigned 097-830446	
PRIORITY DATE CLAIMED 28 October 1998					
TITLE OF INVENTION CHLAMYDIA ANTIGENS AND CORRESPONDING DNA FRAGMENTS AND USES THEREOF					
APPLICANT(S) FOR DO/EO/US Andrew D. MURDIN, Raymond P. OOMEN and Joe WANG					
Applicant herewith submits to the United States Designated/Elected Office (DO/EO/US) the following items and other information:					
1. <input checked="" type="checkbox"/> This is a FIRST submission of items concerning a filing under 35 U.S.C. 371. 2. <input type="checkbox"/> This is a SECOND or SUBSEQUENT submission of items concerning a filing under 35 U.S.C. 371. 3. <input type="checkbox"/> This express request to begin national examination procedures (35 U.S.C. 371(f)) at any time rather than delay examination until the expiration of the applicable time limit set in 35 U.S.C. 371(b) and PCT Articles 22 and 39(1). 4. <input type="checkbox"/> A proper Demand for International Preliminary Examination was made by the 19 <sup>th</sup> month from the earliest claimed priority date. 5. <input checked="" type="checkbox"/> A copy of the International Application as filed (35 U.S.C. 371(c)(2)) <input checked="" type="checkbox"/> is transmitted herewith (required only if not transmitted by the International Bureau). <input type="checkbox"/> has been transmitted by the International Bureau. <input type="checkbox"/> is not required, as the application was filed in the United States Receiving Office (RO/US) 6. <input type="checkbox"/> A translation of the International Application into English (35 U.S.C. 371(c)(2)). 7. <input checked="" type="checkbox"/> Amendments to the claims of the International Application under PCT Article 19 (35 U.S.C. 371(c)(3)) <input type="checkbox"/> are transmitted herewith (required only if not transmitted by the International Bureau). <input type="checkbox"/> have been transmitted by the International Bureau. <input type="checkbox"/> have not been made; however, the time limit for making such amendments has NOT expired. <input checked="" type="checkbox"/> have not been made and will not be made. 8. <input type="checkbox"/> A translation of the amendments to the claims under PCT Article 19 (35 U.S.C. 371(c)(3)). 9. <input type="checkbox"/> An oath or declaration of the inventor(s) (35 U.S.C. 371(c)(4)). 10. <input type="checkbox"/> A translation of the annexes to the International Preliminary Examination Report under PCT Article 36 (35 U.S.C. 371(c)(5)). 11. <input type="checkbox"/> Applicant claims small entity status under 37 CFR 1.27.					
Items 12. to 17. below concern other document(s) or information included:					
12. <input type="checkbox"/> An Information Disclosure Statement under 37 CFR 1.97 and 1.98. 13. <input type="checkbox"/> An assignment document for recording. A separate cover sheet in compliance with 37 CFR 3.28 and 3.31 is included. 14. <input checked="" type="checkbox"/> A FIRST preliminary amendment. <input type="checkbox"/> A SECOND or SUBSEQUENT preliminary amendment. 15. <input type="checkbox"/> A substitute specification. 16. <input type="checkbox"/> A change of power of attorney and/or address letter. 17. <input type="checkbox"/> Other items or information:					

U.S. APPLICATION NO. (if known, see 37 C.F.R. 1.50) To be assigned <b>097830446</b>		INTERNATIONAL APPLICATION NO. PCT/CA99/00992		ATTORNEY'S DOCKET NUMBER 032931/0251	
18. <input checked="" type="checkbox"/> The following fees are submitted:				CALCULATION	
Basic National Fee (37 CFR 1.492(a)(1)-(5): Search Report has been prepared by the EPO or JPO ..... \$860.00					
International preliminary examination fee paid to USPTO (37 CFR 1.482) ..... \$690.00					
No international preliminary examination fee paid to USPTO (37 CFR 1.482) but international search fee paid to USPTO (37 CFR 1.445(a)(2)) ..... \$710.00					
Neither international preliminary examination fee (37 CFR 1.482) nor International search fee (37 CFR 1.445(a)(2)) paid to USPTO ..... \$1,000.00					
International preliminary examination fee paid to USPTO (37 CFR 1.482) and all claims satisfied provisions of PCT Article 33(2)-(4) ..... \$100.00					
ENTER APPROPRIATE BASIC FEE AMOUNT =				\$860.00	
Surcharge of \$130.00 for furnishing the oath or declaration later than 20 Months from the earliest claimed priority date (37 CFR 1.492(e))					
Claims	Number Filed	Included in Basic Fee	Extra Claims	Rate	
Total Claims	39	-	20	= 19	× \$18.00 \$342.00
Independent Claims	8	-	3	= 5	× \$80.00 \$400.00
Multiple dependent claim(s) (if applicable)					\$270.00
TOTAL OF ABOVE CALCULATIONS =				\$1602.00	
Reduction by 1/2 for filing by small entity, if applicable.				\$0.00	
SUBTOTAL =				\$1602.00	
Processing fee of \$130.00 for furnishing English translation later the 20 months from the earliest claimed priority date (37 CFR 1.492(f)).				+	
TOTAL NATIONAL FEE =				\$1602.00	
Fee for recording the enclosed assignment (37 CFR 1.21(h)). The assignment must be accompanied by an appropriate cover sheet (37 CFR 3.28, 3.31). \$40.00 per property				+	
TOTAL FEES ENCLOSED =				\$1602.00	
				Amount to be:	
				refunded \$	
				charged \$	
a. <input checked="" type="checkbox"/> A check in the amount of \$1602.00 to cover the above fees is enclosed. b. <input type="checkbox"/> Please charge my Deposit Account No. <u>19-0741</u> in the amount of \$0.00 to the above fees. A duplicate copy of this sheet is enclosed. c. <input checked="" type="checkbox"/> The Commissioner is hereby authorized to charge any additional fees which may be required, or credit any overpayment to Deposit Account No. <u>19-0741</u> . A duplicate copy of this sheet is enclosed.					
NOTE: Where an appropriate time limit under 37 CFR 1.494 or 1.495 has not been met, a petition to revive (37 CFR 1.137(a) or (b)) must be filed and granted to restore the application to pending status.					
SEND ALL CORRESPONDENCE TO:					
FOLEY & LARDNER 3000 K Street, N.W., Suite 500 Washington, DC 20007			 SIGNATURE NAME BERNHARD D. SAXE REGISTRATION NUMBER 28,665		

RECEIVED 21 SEP 2001

**IN THE UNITED STATES PATENT AND TRADEMARK OFFICE**

Attorney Docket No: 032931/0251

*In re* patent application of  
MURDIN, Andrew D. *et al.*

Serial No.: Not Assigned  
(U.S. Entry of PCT/CA99/00992)

Group Art Unit: Not Assigned

Filed: October 28, 1999 (International Filing Date) Examiner: Not Assigned  
US Entry Date: April 27, 2001

For: CHLAMYDIA ANTIGENS AND CORRESPONDING DNA FRAGMENTS  
AND USES THEREOF

**AMENDMENT ACCOMPANYING SUBMISSION OF SEQUENCE LISTING**

Assistant Commissioner for Patents  
Washington, D.C. 20231

**Box SEQUENCE**

Sir:

In order to comply with the requirements for patent applications containing amino acid and/or sequence disclosures, please amend the application as follows:

**IN THE SPECIFICATION:**

At the end of the specification, please insert the printed Sequence Listing submitted concurrently herewith.

**REMARKS**

Applicants submit this Amendment to insert the required references to SEQ ID NOS of the Sequence Listing filed concurrently herewith, and to indicate the insertion point for the Sequence Listing. Applicants respectfully request examination on the merits of this application.

Respectfully submitted;

Date

June 22, 2001Jay D. Morrow  
Jay D. Morrow  
Reg. No. 30,911

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

Attorney Docket No: 032931/0251

*In re* patent application of  
MURDIN, Andrew D. *et al.*

Serial No.: U.S. National Entry  
of PCT/CA99/00992

Group Art Unit: 1643

Filed: October 28, 1999

Examiner: Not assigned

For: CHLAMYDIA ANTIGENS AND CORRESPONDING DNA FRAGMENTS AND  
USES THEREOF

STATEMENT TO SUPPORT FILING AND SUBMISSION IN  
ACCORDANCE with 37 C.F.R. §§ 1.821-1.825

Assistant Commissioner for Patents  
Washington, D.C. 20231  
**Box SEQUENCE**

Sir:

In connection with a Sequence Listing submitted concurrently herewith,  
the undersigned hereby states that:

1. the submission, filed herewith in accordance with 37 C.F.R. § 1.821(g), does not include new matter; and
2. the content of the attached paper copy and the attached computer readable copy of the Sequence Listing, submitted in accordance with 37 C.F.R. § 1.821(c) and (e), respectively, are the same.

Respectfully submitted,

25 May 2001  
Date

Joy D. Morrow  
Joy D. Morrow  
Reg. No. 30,911



## IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

Applicant: Andrew D. MURDIN  
Title: CHLAMYDIA ANTIGENS AND CORRESPONDING DNA FRAGMENTS  
AND USES THEREOF  
Appl. No.: To be assigned  
Filing Date: April 27, 2001  
Examiner: Unassigned  
Art Unit: Unassigned

**PRELIMINARY AMENDMENT**

Commissioner for Patents  
Washington, D.C. 20231

Sir:

Prior to examination of the above-identified application, Applicants respectfully request that the following amendments be entered into the application:

**IN THE CLAIMS:**

**Please cancel claims 1-24 in their entirety without prejudice or disclaimer and therefore insert new claims 25-63.**

25. (New) A nucleic acid molecule comprising a nucleic acid sequence which encodes a polypeptide selected from any of:

(a) SEQ ID Nos: 27 to 45;

(b) an immunogenic fragment comprising at least 12 consecutive amino acids from a polypeptide of (a); and

(c) a polypeptide of (a) or (b) which has been modified without loss of immunogenicity, wherein said modified polypeptide is at least 75% identical in amino acid sequence to the corresponding polypeptide of (a) or (b).

26. (New) A nucleic acid molecule comprising a nucleic acid sequence selected from any of:

(a) SEQ ID Nos: 1 to 26;

(b) a sequence which encodes a polypeptide encoded by any one of SEQ ID Nos: 1 to 26;

(c) a sequence comprising at least 38 consecutive nucleotides from any one of the nucleic acid sequences of (a) and (b); and

(d) a sequence which encodes a polypeptide which is at least 75% identical in amino acid sequence to any one of the polypeptides encoded by SEQ ID Nos: 1 to 26.

27. (New) A nucleic acid molecule comprising a nucleic acid sequence which is anti-sense to the nucleic acid molecule of claim 25.

28. (New) A nucleic acid molecule comprising a nucleic acid sequence which encodes a fusion protein, said fusion protein comprising a polypeptide encoded by a nucleic acid molecule according to claim 25 and a second polypeptide.

29. (New) The nucleic acid molecule of claim 28 wherein the second polypeptide is a heterologous signal peptide.

30. (New) The nucleic acid molecule of claim 28 wherein the second polypeptide has adjuvant activity.

31. (New) A nucleic acid molecule according to claim 25, operatively linked to one or more expression control sequences.

32. (New) A vaccine comprising a vaccine vector and at least one first nucleic acid selected from any of:

(i) SEQ ID Nos: 1 to 26;

(ii) a nucleic acid sequence which encodes a polypeptide encoded by any one of SEQ ID Nos: 1 to 26;

(iii) a nucleic acid sequence comprising at least 38 consecutive nucleotides from any one of the nucleic acid sequences of (i) and (ii);

(iv) a nucleic acid sequence which encodes a polypeptide which is at least 75% identical in amino acid sequence to the polypeptide encoded by any one of SEQ ID Nos: 1 to 26;

5 (v) a nucleic acid sequence which encodes a polypeptide whose sequence is set forth in any one of SEQ ID Nos: 27 to 45;

(vi) a nucleic acid sequence which encodes an immunogenic fragment comprising at least 12 consecutive amino acids from any one of SEQ ID Nos: 27 to 45; and

10 (vii) a nucleic acid sequence which encodes a polypeptide as defined in (v) or an immunogenic fragment as defined in (vi) which has been modified without loss of immunogenicity, wherein said modified polypeptide or fragment is at least 75% identical in amino acid sequence to the corresponding polypeptide of (v) or the corresponding fragment of (vi);

wherein each first nucleic acid is capable of being expressed.

33. (New) A vaccine comprising a vaccine vector and at least one first nucleic acid  
15 encoding a fusion protein, wherein the fusion protein comprises:

(a) a first polypeptide selected from any of:

(i) a polypeptide encoded by any one of SEQ ID Nos: 1 to 26;

(ii) a polypeptide encoded by a nucleic acid sequence comprising at least 38 consecutive nucleotides from any one of SEQ ID Nos: 1 to 26;

20 (iii) a polypeptide which is at least 75% identical in amino acid sequence to the polypeptide encoded by any one of SEQ ID Nos: 1 to 26;

(iv) a polypeptide whose sequence is set forth in any one of SEQ ID Nos: 27 to 45;

(v) an immunogenic fragment comprising at least 12 consecutive amino acids from any one of SEQ ID Nos: 27 to 45; and

25 (vi) a polypeptide as defined (iv) or an immunogenic fragment as defined in (v) which has been modified without loss of immunogenicity, wherein said modified polypeptide or fragment is at least 75% identical in amino acid sequence to the corresponding polypeptide of (iv) or the corresponding fragment of (v); and

(b) a second polypeptide;

wherein each first nucleic acid is capable of being expressed.

34. (New) The vaccine of claim 33 wherein the second polypeptide is a heterologous signal peptide.

5 35. (New) The vaccine of claim 33 wherein the second polypeptide has adjuvant activity.

36. (New) The vaccine of claim 32 wherein each first nucleic acid is operatively linked to one or more expression control sequences.

37. (New) A vaccine according to claim 32 wherein each first nucleic acid is expressed as a polypeptide, and wherein the vaccine comprises a second nucleic acid encoding an additional  
10 polypeptide which enhances the immune response to the polypeptide expressed by the first nucleic acid.

38. (New) The vaccine of claim 37 wherein the second nucleic acid encodes an additional *Chlamydia* polypeptide.

39. (New) A pharmaceutical composition comprising a nucleic acid according to claim 25  
15 and a pharmaceutically acceptable carrier.

40. (New) A pharmaceutical composition comprising a vaccine according to claim 32 and a pharmaceutically acceptable carrier.

41. (New) A unicellular host transformed with the nucleic acid molecule of claim 31.

42. (New) An isolated nucleic acid probe of 5 to 100 nucleotides which hybridizes under  
20 stringent conditions to any one of nucleic acid molecules of SEQ ID Nos: 1 to 26, or to a complementary or anti-sense sequence of said nucleic acid molecule.

43. (New) A primer of 10 to 40 nucleotides which hybridizes under stringent conditions to any one of nucleic acid molecules of SEQ ID Nos: 1 to 26, or to a homolog or complementary or anti-sense sequence of said nucleic acid molecule.

25 44. (New) A polypeptide encoded by a nucleic acid sequence according to claim 26.

45. (New) A polypeptide comprising an amino acid sequence selected from any of:

(a) SEQ ID Nos: 27 to 45;

(b) an immunogenic fragment comprising at least 12 consecutive amino acids from a polypeptide of (a); and

5 (c) a polypeptide of (a) or (b) which has been modified without loss of immunogenicity, wherein said modified polypeptide is at least 75% identical in amino acid sequence to the corresponding polypeptide of (a) or (b).

46. (New) A fusion protein comprising a polypeptide of claim 44 and a second polypeptide.

10 47. (New) The fusion protein of claim 46 wherein the second polypeptide is a heterologous signal peptide.

48. (New) The fusion protein of claim 46 wherein the second polypeptide has adjuvant activity.

49. (New) A method for producing a polypeptide, comprising the step of culturing a  
15 unicellular host of claim 41 and recovering the resultant polypeptide.

50. (New) An antibody against the polypeptide of claim 44.

51. (New) A vaccine comprising at least one first polypeptide selected from any of:

(i) a polypeptide encoded by any one of SEQ ID Nos: 1 to 26;

(ii) a polypeptide encoded by a nucleic acid sequence comprising at least 38  
20 consecutive nucleotides from any one of SEQ ID Nos: 1 to 26;

(iii) a polypeptide which is at least 75% identical in amino acid sequence to the polypeptide encoded by any one of SEQ ID Nos: 1 to 26;

(iv) a polypeptide whose sequence is set forth in any one of SEQ ID Nos: 27 to 45;

(v) an immunogenic fragment comprising at least 12 consecutive amino acids from  
25 any one of SEQ ID Nos: 27 to 45; and

(vi) a polypeptide as defined in (iv) or an immunogenic fragment as defined in (v) which has been modified without loss of immunogenicity, wherein said modified polypeptide or

52. (New) A vaccine comprising at least one fusion protein, wherein the fusion protein comprises:

(i) a polypeptide encoded by any one of SEQ ID Nos: 1 to 26;

(iii) a polypeptide which is at least 75% identical in amino acid sequence to the

(iv) a polypeptide whose sequence is set forth in any one of SEQ ID Nos: 27 to 45;

(vi) a polypeptide as defined (iv) or an immunogenic fragment as defined in (v)

(b) a second polypeptide.

54. (New) The vaccine of claim 52 wherein the second polypeptide has adjuvant activity.

56. (New) The vaccine of claim 55 wherein the additional polypeptide comprises a *Chlamydia* polypeptide.

57. (New) A pharmaceutical composition comprising a polypeptide according to claim 44 and a pharmaceutically acceptable carrier.

58. (New) A pharmaceutical composition comprising a vaccine according to claim 51 and a pharmaceutically acceptable carrier.

59. (New) A pharmaceutical composition comprising an antibody according to claim 50 and a pharmaceutically acceptable carrier.

5 60. (New) A method for preventing or treating *Chlamydia* infection comprising administering to a patient an effective amount of:

(a) a nucleic acid molecule according to claim 26; or

(b) a vaccine comprising a vaccine vector and at least one first nucleic acid according to claim 26; or

10 (c) a pharmaceutical composition comprising a nucleic acid according to claim 26 and a pharmaceutically acceptable carrier; or

(d) a polypeptide encoded by a nucleic acid sequence according to claim 26; or

(e) an antibody against a polypeptide encoded by a nucleic acid sequence according to claim 26.

15 61. (New) A method of detecting *Chlamydia* infection comprising the step of contacting a body fluid of a mammal to be tested, with a component selected from any one of:

(a) a nucleic acid molecule according to claim 26;

(b) a polypeptide encoded by a nucleic acid sequence according to claim 26; and

20 (c) an antibody against a polypeptide encoded by a nucleic acid sequence according to claim 26.

62. (New) A diagnostic kit comprising instructions for use and a component selected from any one of:

(a) a nucleic acid molecule according to claim 26;

(b) a polypeptide encoded by a nucleic acid sequence according to claim 26; and

25 (c) an antibody against a polypeptide encoded by a nucleic acid sequence according to claim 26.

63. (New) A method for identifying a polypeptide of claim 44 which induces an immune response effective to prevent or lessen the severity of *Chlamydia* infection in a mammal previously immunized with polypeptide, comprising the steps of:

(a) immunizing a mouse with a polypeptide of claim 44; and

(b) inoculating the immunized mouse with *Chlamydia*;

wherein the polypeptide which prevents or lessens the severity of *Chlamydia* infection in the immunized mouse compared to a non-immunized control mouse is identified.



**REMARKS**

5 The Examiner is respectfully requested to enter the above amendment prior to  
examination of the instant application.

Respectfully submitted,

Date April 27, 2001

FOLEY & LARDNER  
Washington Harbour  
3000 K Street, N.W., Suite 500  
Washington, D.C. 20007-5109  
Telephone: (202) 672-5414  
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By 

Bernhard D. Saxe  
Attorney for Applicant  
Registration No. 28,665

TITLE OF INVENTION

CHLAMYDIA ANTIGENS AND CORRESPONDING DNA FRAGMENTS AND USES  
THEREOF

5 REFERENCE TO RELATED APPLICATIONS

This application claims the benefit of U.S. Provisional Application No. 60/106034, filed October 28, 1998, U.S. Provisional Application No. 60/106039, filed October 28, 1998, U.S. Provisional Application No. 60/106042, filed October 28, 1998, U.S. Provisional Application No. 60/106044, filed October 28, 1998, U.S. Provisional Application No. 60/106072, filed October 29, 1998, U.S. Provisional Application No. 60/106073, filed October 29, 1998, U.S. Provisional Application No. 60/106074, filed October 29, 1998, U.S. Provisional Application No. 60/106087, filed October 29, 1998, U.S. Provisional Application No. 60/106587, filed November 2, 1998, U.S. Provisional Application No. 60/106588, filed November 2, 1998, U.S. Provisional Application No. 60/107089, filed November 2, 1998, U.S. Provisional Application No. 60/107034, filed November 2, 1998 and U.S. Provisional Application No. 60/107035, filed November 2, 1998.

FIELD OF INVENTION

The present invention relates to *Chlamydia* antigens and corresponding DNA molecules, which can be used to prevent and treat *Chlamydia* infection in mammals, such as humans.

BACKGROUND OF THE INVENTION

Chlamydiae are prokaryotes. They exhibit morphologic and structural similarities to gram-negative bacteria including a trilaminar outer membrane, which contains lipopolysaccharide and several membrane proteins that are structurally and functionally analogous to proteins found in *E. coli*. They are obligate intra-cellular parasites with a unique biphasic life

cycle consisting of a metabolically inactive but infectious extracellular stage and a replicating but non-infectious intracellular stage. The replicative stage of the life-cycle takes place within a membrane-bound inclusion which sequesters the bacteria away from the cytoplasm of the infected host cell.

*C. pneumoniae* is a common human pathogen, originally described as the TWAR strain of *Chlamydia psittaci* but subsequently recognised to be a new species. *C. pneumoniae* is antigenically, genetically and morphologically distinct from other chlamydia species (*C. trachomatis*, *C. pecorum* and *C. psittaci*). It shows 10% or less DNA sequence homology with either of *C. trachomatis* or *C. psittaci*.

*C. pneumoniae* is a common cause of community acquired pneumonia, only less frequent than *Streptococcus pneumoniae* and *Mycoplasma pneumoniae* (Grayston et al. (1995) Journal of Infectious Diseases 168:1231; Campos et al. (1995) Investigation of Ophthalmology and Visual Science 36:1477). It can also cause upper respiratory tract symptoms and disease, including bronchitis and sinusitis (Grayston et al. (1995) Journal of Infectious Diseases 168:1231; Grayston et al (1990) Journal of Infectious Diseases 161:618; Marrie (1993) Clinical Infectious Diseases. 18:501; Wang et al (1986) Chlamydial infections). Cambridge University Press, Cambridge. p. 329 The great majority of the adult population (over 60%) has antibodies to *C. pneumoniae* (Wang et al (1986) Chlamydial infections. Cambridge University Press, Cambridge. p. 329), indicating past infection which was unrecognized or asymptomatic.

*C. pneumoniae* infection usually presents as an acute respiratory disease (i.e., cough, sore throat, hoarseness, and fever; abnormal chest sounds on auscultation). For most patients, the cough persists for 2 to 6 weeks, and recovery is slow. In approximately 10% of these cases, upper respiratory tract infection is followed by bronchitis or pneumonia. Furthermore, during a *C. pneumoniae* epidemic, subsequent

co-infection with pneumococcus has been noted in about half of these pneumonia patients, particularly in the infirm and the elderly. As noted above, there is more and more evidence that *C. pneumoniae* infection is also linked to diseases other than  
5 respiratory infections.

The reservoir for the organism is presumably people. In contrast to *C. psittaci* infections, there is no known bird or animal reservoir. Transmission has not been clearly defined. It may result from direct contact with secretions, from fomites, or  
10 from airborne spread. There is a long incubation period, which may last for many months. Based on analysis of epidemics, *C. pneumoniae* appears to spread slowly through a population (case-to-case interval averaging 30 days) because infected persons are inefficient transmitters of the organism. Susceptibility to *C.*  
15 *pneumoniae* is universal. Reinfections occur during adulthood, following the primary infection as a child. *C. pneumoniae* appears to be an endemic disease throughout the world, noteworthy for superimposed intervals of increased incidence (epidemics) that persist for 2 to 3 years. *C. trachomatis*  
20 infection does not confer cross-immunity to *C. pneumoniae*. Infections are easily treated with oral antibiotics, tetracycline or erythromycin (2 g/d, for at least 10 to 14 d). A recently developed drug, azithromycin, is highly effective as a single-dose therapy against chlamydial infections.

25 In most instances, *C. pneumoniae* infection is often mild and without complications, and up to 90% of infections are subacute or unrecognized. Among children in industrialized countries, infections have been thought to be rare up to the age of 5 y, although a recent study (E Normann et al, Chlamydia  
30 *pneumoniae* in children with acute respiratory tract infections, Acta Paediatrica, 1998, Vol 87, Iss 1, pp 23-27) has reported that many children in this age group show PCR evidence of infection despite being seronegative, and estimates a prevalence of 17-19% in 2-4 y olds. In developing countries, the

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4

seroprevalence of *C. pneumoniae* antibodies among young children is elevated, and there are suspicions that *C. pneumoniae* may be an important cause of acute lower respiratory tract disease and mortality for infants and children in tropical regions of the world.

From seroprevalence studies and studies of local epidemics, the initial *C. pneumoniae* infection usually happens between the ages of 5 and 20 y. In the USA, for example, there are estimated to be 30,000 cases of childhood pneumonia each year caused by *C. pneumoniae*. Infections may cluster among groups of children or young adults (e.g., school pupils or military conscripts).

*C. pneumoniae* causes 10 to 25% of community-acquired lower respiratory tract infections (as reported from Sweden, Italy, Finland, and the USA). During an epidemic, *C. pneumoniae* infection may account for 50 to 60% of the cases of pneumonia. During these periods, also, more episodes of mixed infections with *S. pneumoniae* have been reported. Reinfection during adulthood is common; the clinical presentation tends to be milder. Based on population seroprevalence studies, there tends to be increased exposure with age, which is particularly evident among men. Some investigators have speculated that a persistent, asymptomatic *C. pneumoniae* infection state is common.

In adults of middle age or older, *C. pneumoniae* infection may progress to chronic bronchitis and sinusitis. A study in the USA revealed that the incidence of pneumonia caused by *C. pneumoniae* in persons younger than 60 years is 1 case per 1,000 persons per year; but in the elderly, the disease incidence rose three-fold. *C. pneumoniae* infection rarely leads to hospitalization, except in patients with an underlying illness.

Of considerable importance is the association of atherosclerosis and *C. pneumoniae* infection. There are several

epidemiological studies showing a correlation of previous infections with *C. pneumoniae* and heart attacks, coronary artery and carotid artery disease (Saikku et al. (1988) Lancet;ii:983; Thom et al. (1992) JAMA 268:68; Linnanmaki et al. (1993),  
5 Circulation 87:1030; Saikku et al. (1992) Annals Internal Medicine 116:273; Melnick et al (1993) American Journal of Medicine 95:499). Moreover, the organisms has been detected in atheromas and fatty streaks of the coronary, carotid, peripheral arteries and aorta (Shor et al. (1992) South African. Medical  
10 Journal 82:158; Kuo et al. (1993) Journal of Infectious Diseases 167:841; Kuo et al. (1993) Arteriosclerosis and Thrombosis 13:1500; Campbell et al (1995) Journal of Infectious Diseases 172:585; Chiu et al. Circulation, 1997 (In Press)). Viable *C. pneumoniae* has been recovered from the coronary and carotid  
15 artery (Ramirez et al (1996) Annals of Internal Medicine 125:979; Jackson et al. Abst. K121, p272, 36<sup>th</sup> ICAAC, 15-18 Sept. 1996, New Orleans). Furthermore, it has been shown that *C. pneumoniae* can induce changes of atherosclerosis in a rabbit model (Fong et al (1997) Journal of Clinical Microbiology  
20 35:48). Taken together, these results indicate that it is highly probable that *C. pneumoniae* can cause atherosclerosis in humans, though the epidemiological importance of chlamydial atherosclerosis remains to be demonstrated.

A number of recent studies have also indicated an  
25 association between *C. pneumoniae* infection and asthma. Infection has been linked to wheezing, asthmatic bronchitis, adult-onset asthma and acute exacerbations of asthma in adults, and small-scale studies have shown that prolonged antibiotic  
30 treatment was effective at greatly reducing the severity of the disease in some individuals (Hahn DL, et al. Evidence for Chlamydia pneumoniae infection in steroid-dependent asthma. Ann Allergy Asthma Immunol. 1998 Jan; 80(1): 45-49.; Hahn DL, et al. Association of Chlamydia pneumoniae IgA antibodies with recently symptomatic asthma. Epidemiol Infect. 1996 Dec;

117(3): 513-517; Bjornsson E, et al. Serology of chlamydia in relation to asthma and bronchial hyperresponsiveness. Scand J Infect Dis. 1996; 28(1): 63-69.; Hahn DL. Treatment of *Chlamydia pneumoniae* infection in adult asthma: a before-after trial. J Fam Pract. 1995 Oct; 41(4): 345-351.; Allegra L, et al. Acute exacerbations of asthma in adults: role of *Chlamydia pneumoniae* infection. Eur Respir J. 1994 Dec; 7(12): 2165-2168.; Hahn DL, et al. Association of *Chlamydia pneumoniae* (strain TWAR) infection with wheezing, asthmatic bronchitis, and adult-onset asthma. JAMA. 1991 Jul 10; 266(2): 225-230).

In light of these results a protective vaccine against *C. pneumoniae* infection would be of considerable importance. There is not yet an effective vaccine for any human chlamydial infection. It is conceivable that an effective vaccine can be developed using physically or chemically inactivated *Chlamydiae*. However, such a vaccine does not have a high margin of safety. In general, safer vaccines are made by genetically manipulating the organism by attenuation or by recombinant means. Accordingly, a major obstacle in creating an effective and safe vaccine against human chlamydial infection has been the paucity of genetic information regarding *Chlamydia*, specifically *C. pneumoniae*.

Studies with *C. trachomatis* and *C. psittaci* indicate that safe and effective vaccine against *Chlamydia* is an attainable goal. For example, mice which have recovered from a lung infection with *C. trachomatis* are protected from infertility induced by a subsequent vaginal challenge (Pal et al. (1996) Infection and Immunity. 64:5341). Similarly, sheep immunized with inactivated *C. psittaci* were protected from subsequent chlamydial-induced abortions and stillbirths (Jones et al. (1995) Vaccine 13:715). Protection from chlamydial infections has been associated with Th1 immune responses, particularly the induction of INF $\gamma$  - producing CD4+T-cells (Igiyetemes et al. (1993) Immunology 5:317). The adoptive

transfer of CD4+ cell lines or clones to nude or SCID mice conferred protection from challenge or cleared chronic disease (Igietseme et al (1993) Regional Immunology 5:317; Magee et al (1993) Regional Immunology 5: 305), and *in vivo* depletion of CD4+ T cells exacerbated disease post-challenge (Landers et al (1991) Infection & Immunity 59:3774; Magee et al (1995) Infection & Immunity 63:516). However, the presence of sufficiently high titres of neutralising antibody at mucosal surfaces can also exert a protective effect (Cotter et al. (1995) Infection and Immunity 63:4704).

Antigenic variation within the species *C. pneumoniae* is not well documented due to insufficient genetic information, though variation is expected to exist based on *C. trachomatis*. Serovars of *C. trachomatis* are defined on the basis of antigenic variation in MOMP, but published *C. pneumoniae* MOMP gene sequences show no variation between several diverse isolates of the organism (Campbell et al (1990) Infection and Immunity 58:93; McCafferty et al (1995) Infection and Immunity 63:2387-9; Knudsen et al (1996) Third Meeting of the European Society for Chlamydia Research, Vienna). Regions of the protein known to be conserved in other chlamydial MOMPs are conserved in *C. pneumoniae* (Campbell et al (1990) Infection and Immunity 58:93; McCafferty et al (1995) Infection and Immunity 63:2387-9). One study has described a strain of *C. pneumoniae* with a MOMP of greater than usual molecular weight, but the gene for this has not been sequenced (Grayston et al. (1995) Journal of Infectious Diseases 168:1231). Partial sequences of outer membrane protein 2 from nine diverse isolates were also found to be invariant (Ramirez et al (1996) Annals of Internal Medicine 125:979). The genes for HSP60 and HSP70 show little variation from other chlamydial species, as would be expected. The gene encoding a 76kDa antigen has been cloned from a single strain of *C. pneumoniae*. It has no significant similarity with other known



chlamydial genes (Marrie (1993) Clinical Infectious Diseases. 18:501).

Many antigens recognised by immune sera to *C. pneumoniae* are conserved across all *Chlamydiae*, but 98kDa, 76kDa and 54kDa proteins appear to be *C. pneumoniae*-specific (Campos et al. (1995) Investigation of Ophthalmology and Visual Science 36:1477; Marrie (1993) Clinical Infectious Diseases. 18:501; Wiedmann-Al-Ahmad M, et al. Reactions of polyclonal and neutralizing anti-p54 monoclonal antibodies with an isolated, species-specific 54-kilodalton protein of *Chlamydia pneumoniae*. Clin Diagn Lab Immunol. 1997 Nov; 4(6): 700-704). A publication relevant to 98KDa proteins is Perez Melgosa et al. FEMS Microbiology Letters. 112(2): 199-204. 1993.

Immunoblotting of isolates with sera from patients does show variation of blotting patterns between isolates, indicating that serotypes *C. pneumoniae* may exist (Ref 1,16). However, the results are potentially confounded by the infection status of the patients, since immunoblot profiles of a patient's sera change with time post-infection. An assessment of the number and relative frequency of any serotypes, and the defining antigens, is not yet possible.

Accordingly, a need exists for identifying and isolating polynucleotide sequences of *C. pneumoniae* for use in preventing and treating *Chlamydia* infection.

## 25 SUMMARY OF THE INVENTION

The present invention provides purified and isolated polynucleotide molecules that encode *Chlamydia* polypeptides which can be used in methods to prevent, treat, and diagnose *Chlamydia* infection. In one form of the invention, the polynucleotide molecules are selected from DNA that encode polypeptides CPN100397 (SEQ ID Nos: 1 and 2), CPN100421 (SEQ ID

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Nos: 3 and 4), CPN100422 (SEQ ID Nos: 5 and 6), CPN100424 (SEQ  
ID Nos: 7 and 8), CPN100426 (SEQ ID Nos: 9 and 10), CPN100506  
(SEQ ID Nos: 11 and 12), CPN100515 (SEQ ID Nos: 13 and 14),  
CPN100538 (SEQ ID Nos: 15 and 16), CPN100557 (SEQ ID Nos: 17  
5 and

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18), CPN100622 (SEQ ID Nos: 19 and 20), CPN100626 (SEQ ID Nos: 21 and, 22), CPN100628 (SEQ ID Nos: 23 and 24) and CPN100630 (SEQ ID Nos: 25 and 26).

Another form of the invention provides polypeptides 5 corresponding to the isolated DNA molecules. The amino acid sequences of the corresponding encoded polypeptides are shown for CPN100397 as SEQ ID Nos: 27 and 28, CPN100421 as SEQ ID No: 29, CPN100422 as SEQ ID No: 30, CPN100424 as SEQ ID No: 31, CPN100426 as SEQ ID No: 32, CPN100508 as SEQ ID Nos: 33 and 34, 10 CPN100515 as SEQ ID Nos: 35 and 36, CPN100538 as SEQ ID No: 37, CPN100557 as SEQ ID Nos: 38 and 39, CPN100622 as SEQ ID Nos: 40 and 41, CPN100626 as SEQ ID No: 42, CPN100628 as SEQ ID No: 43 and CPN100630 as SEQ ID Nos: 44 and 45.

Those skilled in the art will readily understand that the 15 invention, having provided the polynucleotide sequences encoding *Chlamydia* polypeptides, also provides polynucleotides encoding fragments derived from such peptides. Moreover, the invention is understood to provide mutants and derivatives of such polypeptides and fragments derived therefrom, which result from 20 the addition, deletion, or substitution of non-essential amino acids as described herein. Those skilled in the art would also readily understand that the invention, having provided the polynucleotide sequences encoding *Chlamydia* polypeptides, further provides monospecific antibodies that specifically bind 25 to such polypeptides

The present invention has wide application and includes expression cassettes, vectors, and cells transformed or transfected with the polynucleotides of the invention. Accordingly, the present invention further provides (i) a method 30 for producing a polypeptide of the invention in a recombinant host system and related expression cassettes, vectors, and transformed or transfected cells; (ii) a vaccine, or a live vaccine vector such as a pox virus, *Salmonella typhimurium*, or *Vibrio cholerae* vector, containing a polynucleotide of the

invention, such vaccines and vaccine vectors being useful for, e.g., preventing and treating *Chlamydia* infection, in combination with a diluent or carrier, and related pharmaceutical compositions and associated therapeutic and/or prophylactic methods; (iii) a therapeutic and/or prophylactic use of an RNA or DNA molecule of the invention, either in a naked form or formulated with a delivery vehicle, a polypeptide or combination of polypeptides, or a monospecific antibody of the invention, and related pharmaceutical compositions; (iv) a method for diagnosing the presence of *Chlamydia* in a biological sample, which can involve the use of a DNA or RNA molecule, a monospecific antibody, or a polypeptide of the invention; and (v) a method for purifying a polypeptide of the invention by antibody-based affinity chromatography.

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#### BRIEF DESCRIPTION OF THE DRAWINGS

The present invention will be further understood from the following description with reference to the drawings, in which:

Figure 1 shows the nucleotide sequence of the CPN100397 (SEQ ID No: 1 - entire sequence and SEQ ID No: 2 - coding sequence) and the deduced amino acid sequence of the CPN100397 protein from *Chlamydia pneumoniae* (SEQ ID No: 27 and 28).

Figure 2 shows the restriction enzyme analysis of the gene encoding the *C. pneumoniae* CPN100397 gene.

25 Figure 3 shows the nucleotide sequence of the CPN100421 (SEQ ID No: 3 - entire sequence and SEQ ID No: 4 - coding sequence) and the deduced amino acid sequence of the CPN100421 protein from *Chlamydia pneumoniae* (SEQ ID No: 29).

Figure 4 shows the restriction enzyme analysis of the 30 gene encoding the *C. pneumoniae* CPN100421 gene.

Figure 5 shows the nucleotide sequence of the CPN100422 (SEQ ID No: 5 - entire sequence and SEQ ID No: 6 - coding sequence) and the deduced amino acid sequence of the CPN100422 protein from *Chlamydia pneumoniae* (SEQ ID No: 30).

Figure 6 shows the restriction enzyme analysis of the gene encoding the *C. pneumoniae* CPN100422 gene.

Figure 7 shows the nucleotide sequence of the CPN100424 (SEQ ID No: 7 - entire sequence and SEQ ID No: 8 - coding 5 sequence) and the deduced amino acid sequence of the CPN100424 protein from *Chlamydia pneumoniae* (SEQ ID No: 31).

Figure 8 shows the restriction enzyme analysis of the gene encoding the *C. pneumoniae* CPN100424 gene.

Figure 9 shows the nucleotide sequence of the CPN100426 10 (SEQ ID No: 9 - entire sequence and SEQ ID No: 10 - coding sequence) and the deduced amino acid sequence of the CPN100426 protein from *Chlamydia pneumoniae* (SEQ ID No: 32).

Figure 10 shows the restriction enzyme analysis of the gene encoding the *C. pneumoniae* CPN100426 gene.

Figure 11 shows the nucleotide sequence of the CPN100508 15 (SEQ ID No: 11 - entire sequence and SEQ ID No: 12 - coding sequence) and the deduced amino acid sequence of the CPN100508 protein from *Chlamydia pneumoniae* (SEQ ID No: 33 - full length sequence and SEQ ID No: 34 - processed sequence).

Figure 12 shows the restriction enzyme analysis of the 20 gene encoding the *C. pneumoniae* CPN100508 gene.

Figure 13 shows the nucleotide sequence of the CPN100515 (SEQ ID No: 13 - entire sequence and SEQ ID No: 14 - coding sequence) and the deduced amino acid sequence of the CPN100515 25 protein from *Chlamydia pneumoniae* (SEQ ID No: 35 - full length sequence and SEQ ID No: 36 - processed sequence).

Figure 14 shows the restriction enzyme analysis of the gene encoding the *C. pneumoniae* CPN100515 gene.

Figure 15 shows the nucleotide sequence of the CPN100538 30 (SEQ ID No: 15 - entire sequence and SEQ ID No: 16 - coding sequence) and the deduced amino acid sequence of the CPN100538 protein from *Chlamydia pneumoniae* (SEQ ID No: 37).

Figure 16 shows the restriction enzyme analysis of the gene encoding the *C. pneumoniae* CPN100538 gene.

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Figure 17 shows the nucleotide sequence of the CPN100557 (SEQ ID No: 17 - entire sequence and SEQ ID No: 18 - coding sequence) and the deduced amino acid sequence of the CPN100557 protein from *Chlamydia pneumoniae* (SEQ ID No: 38 - full length sequence and SEQ ID No: 39 - processed sequence).

Figure 18 shows the restriction enzyme analysis of the gene encoding the *C. pneumoniae* CPN100557 gene.

Figure 19 shows the nucleotide sequence of the CPN100622 (SEQ ID No: 19 - entire sequence and SEQ ID No: 20 - coding sequence) and the deduced amino acid sequence of the CPN100622 protein from *Chlamydia pneumoniae* (SEQ ID No: 40 - full length sequence and SEQ ID No: 41 - processed sequence).

Figure 20 shows the restriction enzyme analysis of the gene encoding the *C. pneumoniae* CPN100622 gene.

Figure 21 shows the nucleotide sequence of the CPN100626 (SEQ ID No: 21 - entire sequence and SEQ ID No: 22 - coding sequence) and the deduced amino acid sequence of the CPN100626 protein from *Chlamydia pneumoniae* (SEQ ID No: 42).

Figure 22 shows the restriction enzyme analysis of the gene encoding the *C. pneumoniae* CPN100626 gene.

Figure 23 shows the nucleotide sequence of the CPN100628 (SEQ ID No: 23 - entire sequence and SEQ ID No: 24 - coding sequence) and the deduced amino acid sequence of the CPN100628 protein from *Chlamydia pneumoniae* (SEQ ID No: 43).

Figure 24 shows the restriction enzyme analysis of the gene encoding the *C. pneumoniae* CPN100628 gene.

Figure 25 shows the nucleotide sequence of the CPN100630 (SEQ ID No: 25 - entire sequence and SEQ ID No: 26 - coding sequence) and the deduced amino acid sequence of the CPN100630 protein from *Chlamydia pneumoniae* (SEQ ID No: 44 - full length sequence and SEQ ID No: 45 - processed sequence).

Figure 26 shows the restriction enzyme analysis of the gene encoding the *C. pneumoniae* CPN100630 gene.

Figures 27 through 39 show an identification of T and B cell epitopes from the amino acid sequences shown in the foregoing figures.

## 5 DETAILED DESCRIPTION OF INVENTION

Open reading frames (ORFs) encoding chlamydial polypeptides have been identified from the *C. pneumoniae* genome. These polypeptides include polypeptides found permanently in the bacterial membrane structure, polypeptides present in the  
10 external vicinity of the bacterial membrane, polypeptides found permanently in the inclusion membrane structure, polypeptides present in the external vicinity of the inclusion membrane, and polypeptides released into the cytoplasm of the infected cell. These polypeptides can be used to prevent and treat *Chlamydia*  
15 infection.

According to a first aspect of the invention, isolated polynucleotides are provided which encode the precursor and mature forms of *Chlamydia* polypeptides, whose amino acid sequences are selected from the group consisting of: SEQ ID  
20 Nos: 27 to 45.

The term "isolated polynucleotide" is defined as a polynucleotide removed from the environment in which it naturally occurs. For example, a naturally-occurring DNA molecule present in the genome of a living bacteria or as part  
25 of a gene bank is not isolated, but the same molecule separated from the remaining part of the bacterial genome, as a result of, e.g., a cloning event (amplification), is isolated. Typically, an isolated DNA molecule is free from DNA regions (e.g., coding regions) with which it is immediately contiguous at the 5' or 3'  
30 end, in the naturally occurring genome. Such isolated polynucleotides may be part of a vector or a composition and still be defined as isolated in that such a vector or composition is not part of the natural environment of such polynucleotide.

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The polynucleotide of the invention is either RNA or DNA (cDNA, genomic DNA, or synthetic DNA), or modifications, variants, homologs or fragments thereof. The DNA is either double-stranded or single-stranded, and, if single-stranded, is either the coding strand or the non-coding (anti-sense) strand. Any one of the sequences that encode the polypeptides of the invention as shown in SEQ ID Nos: 1 to 26 is (a) a coding sequence, (b) a ribonucleotide sequence derived from transcription of (a), or (c) a coding sequence which uses the redundancy or degeneracy of the genetic code to encode the same polypeptides. By "polypeptide" or "protein" is meant any chain of amino acids, regardless of length or post-translational modification (e.g., glycosylation or phosphorylation). Both terms are used interchangeably in the present application.

Consistent with the first aspect of the invention, amino acid sequences are provided which are homologous to any one of SEQ ID Nos: 27 to 45. As used herein, "homologous amino acid sequence" is any polypeptide which is encoded, in whole or in part, by a nucleic acid sequence which hybridizes at 25-35°C below critical melting temperature ( $T_m$ ), to any portion of the nucleic acid sequences of SEQ ID Nos: 1 to 26. A homologous amino acid sequence is one that differs from an amino acid sequence shown in any one of SEQ ID Nos: 27 to 45 by one or more amino acid substitutions. Such a sequence also encompasses serotypic variants (defined below) as well as sequences containing deletions or insertions which retain inherent characteristics of the polypeptide such as immunogenicity. Preferably, such a sequence is at least 75%, more preferably 80%, and most preferably 90% identical to any one of SEQ ID Nos: 27 to 45. Homologous amino acid sequences include sequences that are identical or substantially identical to SEQ ID Nos: 27 to 45. By "amino acid sequence substantially identical" is meant a sequence that is at least 90%, preferably 95%, more preferably 97%, and most preferably 99% identical to



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an amino acid sequence of reference and that preferably differs from the sequence of reference by a majority of conservative amino acid substitutions.

Conservative amino acid substitutions are substitutions among amino acids of the same class. These classes include, for example, amino acids having uncharged polar side chains, such as asparagine, glutamine, serine, threonine, and tyrosine; amino acids having basic side chains, such as lysine, arginine, and histidine; amino acids having acidic side chains, such as aspartic acid and glutamic acid; and amino acids having nonpolar side chains, such as glycine, alanine, valine, leucine, isoleucine, proline, phenylalanine, methionine, tryptophan, and cysteine.

Homology is measured using sequence analysis software such as Sequence Analysis Software Package of the Genetics Computer Group, University of Wisconsin Biotechnology Center, 1710 University Avenue, Madison, WI 53705. Amino acid sequences are aligned to maximize identity. Gaps may be artificially introduced into the sequence to attain proper alignment. Once the optimal alignment has been set up, the degree of homology is established by recording all of the positions in which the amino acids of both sequences are identical, relative to the total number of positions.

Homologous polynucleotide sequences are defined in a similar way. Preferably, a homologous sequence is one that is at least 45%, more preferably 60%, and most preferably 85% identical to any one of coding sequences SEQ ID Nos: 1 to 26.

Consistent with the first aspect of the invention, polypeptides having a sequence homologous to any one of SEQ ID Nos: 27 to 45 include naturally-occurring allelic variants, as well as mutants or any other non-naturally occurring variants that retain the inherent characteristics of the polypeptide of SEQ ID Nos: 27 to 45.

As is known in the art, an allelic variant is an alternate form of a polypeptide that is characterized as having a substitution, deletion, or addition of one or more amino acids that does not alter the biological function of the polypeptide.

5 By "biological function" is meant the function of the polypeptide in the cells in which it naturally occurs, even if the function is not necessary for the growth or survival of the cells. For example, the biological function of a porin is to allow the entry into cells of compounds present in the  
10 extracellular medium. Biological function is distinct from antigenic property. A polypeptide can have more than one biological function.

Allelic variants are very common in nature. For example, a bacterial species such as *C. pneumoniae*, is usually  
15 represented by a variety of strains that differ from each other by minor allelic variations. Indeed, a polypeptide that fulfills the same biological function in different strains can have an amino acid sequence (and polynucleotide sequence) that are not identical in each of the strains. Despite this  
20 variation, an immune response directed generally against many allelic variants has been demonstrated. In studies of the *Chlamydial* MOMP antigen, cross-strain antibody binding plus neutralization of infectivity occurs despite amino acid sequence variation of MOMP from strain to strain, indicating that the  
25 MOMP, when used as an immunogen, is tolerant of amino acid variations.

Polynucleotides encoding homologous polypeptides or allelic variants are retrieved by polymerase chain reaction (PCR) amplification of genomic bacterial DNA extracted by  
30 conventional methods. This involves the use of synthetic oligonucleotide primers matching upstream and downstream of the 5' and 3' ends of the encoding domain. Suitable primers are designed according to the nucleotide sequence information provided in SEQ ID Nos:1 to 26. The procedure is as follows: a

primer is selected which consists of 10 to 40, preferably 15 to 25 nucleotides. It is advantageous to select primers containing C and G nucleotides in a proportion sufficient to ensure efficient hybridization; i.e., an amount of C and G nucleotides 5 of at least 40%, preferably 50% of the total nucleotide content.

An alternative method for retrieving polynucleotides encoding homologous polypeptides or allelic variants is by hybridization screening of a DNA or RNA library. Hybridization procedures are well-known in the art and are described in 10 Ausubel *et al.*, (Ref 41), Silhavy *et al.* (Ref 43), and Davis *et al.* (ref 44). Important parameters for optimizing hybridization conditions are reflected in a formula used to obtain the critical melting temperature above which two complementary DNA strands separate from each other (Ref 45). For polynucleotides 15 of about 600 nucleotides or larger, this formula is as follows:  
$$T_m = 81.5 + 0.5 \times (\% \text{ G+C}) + 1.6 \log (\text{positive ion concentration}) - 0.6 \times (\% \text{ formamide}).$$
  
Under appropriate stringency conditions, hybridization temperature ( $T_h$ ) is approximately 20 to 40°C, 20 to 25°C, or, preferably 30 to 40°C below the calculated  $T_m$ .  
20 Those skilled in the art will understand that optimal temperature and salt conditions can be readily determined.

For the polynucleotides of the invention, stringent conditions are achieved for both pre-hybridizing and hybridizing incubations (i) within 4-16 hours at 42°C, in 6 x SSC containing 25 50% formamide, or (ii) within 4-16 hours at 65°C in an aqueous 6 x SSC solution (1 M NaCl, 0.1 M sodium citrate (pH 7.0)).

Useful homologs and fragments thereof that do not occur naturally are designed using known methods for identifying regions of an antigen that are likely to tolerate amino acid 30 sequence changes and/or deletions. As an example, homologous polypeptides from different species are compared; conserved sequences are identified. The more divergent sequences are the most likely to tolerate sequence changes. Alternatively, sequences are modified such that they become more reactive to T-

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and/or B-cells. (See Table below for identification of T- and B- epitopes.) Yet another alternative is to mutate a particular amino acid residue or sequence within the polypeptide *in vitro*, then screen the mutant polypeptides for their ability to prevent  
5 or treat Chlamydia infection according to the method outlined below.

A person skilled in the art will readily understand that by following the screening process of this invention, it will be determined without undue experimentation whether a particular  
10 homolog of any of SEQ ID Nos: 27 to 45 may be useful in the prevention or treatment of Chlamydia infection. The screening procedure comprises the steps:

- (i) immunizing an animal, preferably mouse, with the test homolog or fragment;
- 15 (ii) inoculating the immunized animal with Chlamydia; and
- (iii) selecting those homologs or fragments which confer protection against Chlamydia.

By "conferring protection" is meant that there is a  
20 reduction in severity of any of the effects of Chlamydia infection, in comparison with a control animal which was not immunized with the test homolog or fragment.

It has been previously demonstrated (Yang et. al., 1993) that mice are susceptible to intranasal infection with different  
25 isolates of *C. pneumoniae*. Strain AR-39 (Grayston, 1989) was used in Balb/c mice as a challenge infection model to examine the capacity of chlamydia gene products delivered as naked DNA to elicit a protective response against a sublethal *C. pneumoniae* lung infection. Protective immunity is defined as an  
30 accelerated clearance of pulmonary infection.

Groups of 7 to 9 week old male Balb/c mice (6 to 10 per group) were immunized intramuscularly (i.m.) plus intranasally (i.n.) with plasmid DNA containing the coding sequence of a *C.pneumoniae* polypeptide. Saline or the plasmid vector lacking

an inserted chlamydial gene was given to groups of control animals.

For i.m. immunization alternate left and right quadriceps were injected with 100µg of DNA in 50µl of PBS on three occasions at 0, 3 and 6 weeks. For i.n. immunization, anaesthetized mice aspirated 50µl of PBS containing 50 µg DNA on three occasions at 0, 3 and 6 weeks. At week 8, immunized mice were inoculated i.n. with  $5 \times 10^5$  IFU of *C. pneumoniae*, strain AR39 in 100µl of SPG buffer to test their ability to limit the growth of a sublethal *C. pneumoniae* challenge.

Lungs were taken from mice at day 9 post-challenge and immediately homogenised in SPG buffer (7.5% sucrose, 5mM glutamate, 12.5mM phosphate pH7.5). The homogenate was stored frozen at -70°C until assay. Dilutions of the homogenate were assayed for the presence of infectious chlamydia by inoculation onto monolayers of susceptible cells. The inoculum was centrifuged onto the cells at 3000rpm for 1 hour, then the cells were incubated for three days at 35°C in the presence of 1µg/ml cycloheximide. After incubation the monolayers were fixed with formalin and methanol then immunoperoxidase stained for the presence of chlamydial inclusions using convalescent sera from rabbits infected with *C.pneumoniae* and metal-enhanced DAB as a peroxidase substrate.

Consistent with the first aspect of the invention, polypeptide derivatives are provided that are partial sequences of SEQ ID Nos: 27 to 45, partial sequences of polypeptide sequences homologous to SEQ ID Nos: 27 to 45, polypeptides derived from full-length polypeptides by internal deletion, and fusion proteins.

It is an accepted practice in the field of immunology to use fragments and variants of protein immunogens as vaccines, as all that is required to induce an immune response to a protein is a small (e.g., 8 to 10 amino acid) immunogenic region of the

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protein. Various short synthetic peptides corresponding to surface-exposed antigens of pathogens other than *Chlamydia* have been shown to be effective vaccine antigens against their respective pathogens, e.g. an 11 residue peptide of murine mammary tumor virus (Ref 38), a 16-residue peptide of Semliki Forest virus (Ref 39), and two overlapping peptides of 15 residues each from canine parvovirus (Ref 40).

Accordingly, it will be readily apparent to one skilled in the art, having read the present description, that partial sequences of SEQ ID Nos: 27 to 45 or their homologous amino acid sequences are inherent to the full-length sequences and are taught by the present invention. Such polypeptide fragments preferably are at least 12 amino acids in length. Advantageously, they are at least 20 amino acids, preferably at least 50 amino acids, more preferably at least 75 amino acids, and most preferably at least 100 amino acids in length.

Polynucleotides of 30 to 600 nucleotides encoding partial sequences of sequences homologous to SEQ ID Nos: 27 to 45 are retrieved by PCR amplification using the parameters outlined above and using primers matching the sequences upstream and downstream of the 5' and 3' ends of the fragment to be amplified. The template polynucleotide for such amplification is either the full length polynucleotide homologous to one of SEQ ID Nos: 1 to 26, or a polynucleotide contained in a mixture of polynucleotides such as a DNA or RNA library. As an alternative method for retrieving the partial sequences, screening hybridization is carried out under conditions described above and using the formula for calculating  $T_m$ . Where fragments of 30 to 600 nucleotides are to be retrieved, the calculated  $T_m$  is corrected by subtracting (600/polynucleotide size in base pairs) and the stringency conditions are defined by a hybridization temperature that is 5 to 10°C below  $T_m$ . Where oligonucleotides shorter than 20-30 bases are to be obtained, the formula for calculating the  $T_m$  is as follows:  $T_m = 4 \times (G+C)$

+ 2 (A+T). For example, an 18 nucleotide fragment of 50% G+C would have an approximate  $T_m$  of 54°C. Short peptides that are fragments of SEQ. ID Nos. 27 to 45 or their homologous sequences, are obtained directly by chemical synthesis (E. Gross and H. J. Meinhofer, 4 The Peptides: Analysis, Synthesis, Biology; Modern Techniques of Peptide Synthesis, John Wiley & Sons (1981), and M. Bodanzki, Principles of Peptide Synthesis, Springer-Verlag (1984)).

Useful polypeptide derivatives, e.g., polypeptide fragments, are designed using computer-assisted analysis of amino acid sequences. This identifies probable surface-exposed, antigenic regions (Ref 37). An analysis of the 13 amino acid sequences contained in SEQ ID Nos: 27 to 45, based on the product of flexibility and hydrophobicity propensities using the program SEQSEE (Wishart DS, et al. "SEQSEE: a comprehensive program suite for protein sequence analysis." *Comput Appl Biosci*. 1994 Apr;10(2):121-32), reveal a number of potential B- and T-cell epitopes which may be used as a basis for selecting useful immunogenic fragments and variants. The results are shown in Figures 27 to 39. This analysis uses a reasonable combination of external surface features that is likely to be recognized by antibodies. Probable T-cell epitopes for HLA-A0201 MHC subclass were revealed by an algorithm written at Connaught Laboratories that emulates an approach developed at the NIH (Parker KC, et al. "Peptide binding to MHC class I molecules: implications for antigenic peptide prediction." *Immunol Res* 1995;14(1):34-57 ).

Epitopes which induce a protective T cell-dependent immune response are present throughout the length of the polypeptide. However, some epitopes may be masked by secondary and tertiary structures of the polypeptide. To reveal such masked epitopes large internal deletions are created which remove much of the original protein structure and exposes the masked epitopes. Such internal deletions sometimes effects the

additional advantage of removing immunodominant regions of high variability among strains. Polynucleotides encoding polypeptide fragments and polypeptides having large internal deletions are constructed using standard methods (Ref 41). Such methods  
5 include standard PCR, inverse PCR, restriction enzyme treatment of cloned DNA molecules, or the method of Kunkel et al. (Ref 42). Components for these methods and instructions for their use are readily available from various commercial sources such as Stratagene. Once the deletion mutants have been constructed,  
10 they are tested for their ability to prevent or treat Chlamydia infection as described above.

As used herein, a fusion polypeptide is one that contains a polypeptide or a polypeptide derivative of the invention fused at the N- or C-terminal end to any other polypeptide  
15 (hereinafter referred to as a peptide tail). A simple way to obtain such a fusion polypeptide is by translation of an in-frame fusion of the polynucleotide sequences, i.e., a hybrid gene. The hybrid gene encoding the fusion polypeptide is inserted into an expression vector which is used to transform or  
20 transfect a host cell. Alternatively, the polynucleotide sequence encoding the polypeptide or polypeptide derivative is inserted into an expression vector in which the polynucleotide encoding the peptide tail is already present. Such vectors and instructions for their use are commercially available, e.g.  
25 the pMal-c2 or pMal-p2 system from New England Biolabs, in which the peptide tail is a maltose binding protein, the glutathione-S-transferase system of Pharmacia, or the His-Tag system available from Novagen. These and other expression systems provide convenient means for further purification of  
30 polypeptides and derivatives of the invention.

An advantageous example of a fusion polypeptide is one where the polypeptide or homolog or fragment of the invention is fused to a polypeptide having adjuvant activity, such as subunit B of either cholera toxin or *E. coli* heat-labile toxin. Another



advantageous fusion is one where the polypeptide, homolog or fragment is fused to a strong T-cell epitope or B-cell epitope. Such an epitope may be one known in the art (e.g. the Hepatitis B virus core antigen, D.R. Millich et al., "Antibody production 5 to the nucleocapsid and envelope of the Hepatitis B virus primed by a single synthetic T cell site", Nature. 1987. 329:547-549), or one which has been identified in another polypeptide of the invention (Table ). Consistent with this aspect of the invention is a fusion polypeptide comprising T- or B-cell 10 epitopes from one of SEQ ID Nos: 27 to 45 or its homolog or fragment, wherein the epitopes are derived from multiple variants of said polypeptide or homolog or fragment, each variant differing from another in the location and sequence of its epitope within the polypeptide. Such a fusion is effective 15 in the prevention and treatment of Chlamydia infection since it optimizes the T- and B-cell response to the overall polypeptide, homolog or fragment.

To effect fusion, the polypeptide of the invention is fused to the N-, or preferably, to the C-terminal end of the 20 polypeptide having adjuvant activity or T- or B-cell epitope. Alternatively, a polypeptide fragment of the invention is inserted internally within the amino acid sequence of the polypeptide having adjuvant activity. The T- or B-cell epitope may also be inserted internally within the amino acid sequence 25 of the polypeptide of the invention.

Consistent with the first aspect, the polynucleotides of the invention also encode hybrid precursor polypeptides containing heterologous signal peptides, which mature into polypeptides of the invention. By "heterologous signal peptide" 30 is meant a signal peptide that is not found in naturally-occurring precursors of polypeptides of the invention.

A polynucleotide molecule according to the invention, including RNA, DNA, or modifications or combinations thereof, have various applications. A DNA molecule is used, for example,

(i) in a process for producing the encoded polypeptide in a recombinant host system, (ii) in the construction of vaccine vectors such as poxviruses, which are further used in methods and compositions for preventing and/or treating *Chlamydia*

- 5 infection, (iii) as a vaccine agent (as well as an RNA molecule), in a naked form or formulated with a delivery vehicle and, (iv) in the construction of attenuated *Chlamydia* strains that can over-express a polynucleotide of the invention or express it in a non-toxic, mutated form.

10 Accordingly, a second aspect of the invention encompasses

(i) an expression cassette containing a DNA molecule of the invention placed under the control of the elements required for expression, in particular under the control of an appropriate promoter; (ii) an expression vector containing an expression

- 15 cassette of the invention; (iii) a procaryotic or eucaryotic cell transformed or transfected with an expression cassette and/or vector of the invention, as well as (iv) a process for producing a polypeptide or polypeptide derivative encoded by a polynucleotide of the invention, which involves culturing a
- 20 procaryotic or eucaryotic cell transformed or transfected with an expression cassette and/or vector of the invention, under conditions that allow expression of the DNA molecule of the invention and, recovering the encoded polypeptide or polypeptide derivative from the cell culture.

- 25 A recombinant expression system is selected from procaryotic and eucaryotic hosts. Eucaryotic hosts include yeast cells (e.g., *Saccharomyces cerevisiae* or *Pichia pastoris*), mammalian cells (e.g., COS1, NIH3T3, or JEG3 cells), arthropods cells (e.g., *Spodoptera frugiperda* (SF9) cells), and plant
- 30 cells. A preferred expression system is a procaryotic host such as *E. coli*. Bacterial and eucaryotic cells are available from a number of different sources including commercial sources to those skilled in the art, e.g., the American Type Culture Collection (ATCC; Rockville, Maryland). Commercial sources of

cells used for recombinant protein expression also provide instructions for usage of the cells.

The choice of the expression system depends on the features desired for the expressed polypeptide. For example, it may be useful to produce a polypeptide of the invention in a particular lipidated form or any other form.

One skilled in the art would readily understand that not all vectors and expression control sequences and hosts would be expected to express equally well the polynucleotides of this invention. With the guidelines described below, however, a selection of vectors, expression control sequences and hosts may be made without undue experimentation and without departing from the scope of this invention.

In selecting a vector, the host must be chosen that is compatible with the vector which is to exist and possibly replicate in it. Considerations are made with respect to the vector copy number, the ability to control the copy number, expression of other proteins such as antibiotic resistance. In selecting an expression control sequence, a number of variables are considered. Among the important variable are the relative strength of the sequence (e.g. the ability to drive expression under various conditions), the ability to control the sequence's function, compatibility between the polynucleotide to be expressed and the control sequence (e.g. secondary structures are considered to avoid hairpin structures which prevent efficient transcription). In selecting the host, unicellular hosts are selected which are compatible with the selected vector, tolerant of any possible toxic effects of the expressed product, able to secrete the expressed product efficiently if such is desired, to be able to express the product in the desired conformation, to be easily scaled up, and to which ease of purification of the final product.

The choice of the expression cassette depends on the host system selected as well as the features desired for the

expressed polypeptide. Typically, an expression cassette includes a promoter that is functional in the selected host system and can be constitutive or inducible; a ribosome binding site; a start codon (ATG) if necessary; a region encoding a signal peptide, e.g., a lipidation signal peptide; a DNA molecule of the invention; a stop codon; and optionally a 3' terminal region (translation and/or transcription terminator). The signal peptide encoding region is adjacent to the polynucleotide of the invention and placed in proper reading frame. The signal peptide-encoding region is homologous or heterologous to the DNA molecule encoding the mature polypeptide and is compatible with the secretion apparatus of the host used for expression. The open reading frame constituted by the DNA molecule of the invention, solely or together with the signal peptide, is placed under the control of the promoter so that transcription and translation occur in the host system. Promoters and signal peptide encoding regions are widely known and available to those skilled in the art and include, for example, the promoter of *Salmonella typhimurium* (and derivatives) that is inducible by arabinose (promoter araB) and is functional in Gram-negative bacteria such as *E. coli* (as described in U.S. Patent No. 5,028,530 and in Cagnon et al., (Ref 46)); the promoter of the gene of bacteriophage T7 encoding RNA polymerase, that is functional in a number of *E. coli* strains expressing T7 polymerase (described in U.S. Patent No. 4,952,496); OspA lipidation signal peptide; and RlpB lipidation signal peptide (Ref 47).

The expression cassette is typically part of an expression vector, which is selected for its ability to replicate in the chosen expression system. Expression vectors (e.g., plasmids or viral vectors) can be chosen, for example, from those described in Pouwels et al. (Cloning Vectors: A Laboratory Manual 1985, Supp. 1987). Suitable expression vectors can be purchased from various commercial sources.

Methods for transforming/transfecting host cells with expression vectors are well-known in the art and depend on the host system selected as described in Ausubel et al., (Ref 41).

Upon expression, a recombinant polypeptide of the invention (or a polypeptide derivative) is produced and remains in the intracellular compartment, is secreted/excreted in the extracellular medium or in the periplasmic space, or is embedded in the cellular membrane. The polypeptide is recovered in a substantially purified form from the cell extract or from the supernatant after centrifugation of the recombinant cell culture. Typically, the recombinant polypeptide is purified by antibody-based affinity purification or by other well-known methods that can be readily adapted by a person skilled in the art, such as fusion of the polynucleotide encoding the polypeptide or its derivative to a small affinity binding domain. Antibodies useful for purifying by immunoaffinity the polypeptides of the invention are obtained as described below.

A polynucleotide of the invention can also be useful as a vaccine. There are two major routes, either using a viral or bacterial host as gene delivery vehicle (live vaccine vector) or administering the gene in a free form, e.g., inserted into a plasmid. Therapeutic or prophylactic efficacy of a polynucleotide of the invention is evaluated as described below.

Accordingly, a third aspect of the invention provides (i) a vaccine vector such as a poxvirus, containing a DNA molecule of the invention, placed under the control of elements required for expression; (ii) a composition of matter comprising a vaccine vector of the invention, together with a diluent or carrier; specifically (iii) a pharmaceutical composition containing a therapeutically or prophylactically effective amount of a vaccine vector of the invention; (iv) a method for inducing an immune response against *Chlamydia* in a mammal (e.g., a human; alternatively, the method can be used in veterinary applications for treating or preventing *Chlamydia* infection of

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animals, e.g., cats or birds), which involves administering to the mammal an immunogenically effective amount of a vaccine vector of the invention to elicit a protective or therapeutic immune response to *Chlamydia* ; and particularly, (v) a method  
5 for preventing and/or treating a *Chlamydia* (e.g., *C. trachomatis*, *C. psittaci*, *C. pneumonia*, *C. pecorum*) infection, which involves administering a prophylactic or therapeutic amount of a vaccine vector of the invention to an infected individual. Additionally, the third aspect of the invention  
10 encompasses the use of a vaccine vector of the invention in the preparation of a medicament for preventing and/or treating *Chlamydia* infection.

As used herein, a vaccine vector expresses one or several polypeptides or derivatives of the invention, as well as at  
15 least one additional *Chlamydia* antigen (??), fragment, homolog, mutant, or derivative thereof. The vaccine vector may express additionally a cytokine, such as interleukin-2 (IL-2) or interleukin-12 (IL-12), that enhances the immune response (adjuvant effect). It is understood that each of the components  
20 to be expressed is placed under the control of elements required for expression in a mammalian cell.

Consistent with the third aspect of the invention is a composition comprising several vaccine vectors, each of them capable of expressing a polypeptide or derivative of the  
25 invention. A composition may also comprise a vaccine vector capable of expressing an additional *Chlamydia* antigen, or a subunit, fragment, homolog, mutant, or derivative thereof; or a cytokine such as IL-2 or IL-12.

Vaccination methods for treating or preventing infection  
30 in a mammal comprises use of a vaccine vector of the invention to be administered by any conventional route , particularly to a mucosal (e.g., ocular, intranasal, oral, gastric, pulmonary, intestinal, rectal, vaginal, or urinary tract) surface or via the parenteral (e.g., subcutaneous, intradermal, intramuscular,

intravenous, or intraperitoneal) route. Preferred routes depend upon the choice of the vaccine vector. Treatment may be effected in a single dose or repeated at intervals. The appropriate dosage depends on various parameters understood by skilled artisans such as the vaccine vector itself, the route of administration or the condition of the mammal to be vaccinated (weight, age and the like).

Live vaccine vectors available in the art include viral vectors such as adenoviruses and poxviruses as well as bacterial vectors, e.g., *Shigella*, *Salmonella*, *Vibrio cholerae*, *Lactobacillus*, Bacille bilié de Calmette-Guérin (BCG), and *Streptococcus*.

An example of an adenovirus vector, as well as a method for constructing an adenovirus vector capable of expressing a DNA molecule of the invention, are described in U.S. Patent No. 4,920,209. Poxvirus vectors include vaccinia and canary pox virus, described in U.S. Patent No. 4,722,848 and U.S. Patent No. 5,364,773, respectively. (Also see, e.g., Tartaglia et al., Virology (1992) 188:217) for a description of a vaccinia virus vector and Taylor et al, Vaccine (1995) 13:539 for a reference of a canary pox.) Poxvirus vectors capable of expressing a polynucleotide of the invention are obtained by homologous recombination as described in Kieny et al., Nature (1984) 312:163 so that the polynucleotide of the invention is inserted in the viral genome under appropriate conditions for expression in mammalian cells. Generally, the dose of vaccine viral vector, for therapeutic or prophylactic use, can be of from about  $1 \times 10^4$  to about  $1 \times 10^{11}$ , advantageously from about  $1 \times 10^7$  to about  $1 \times 10^{10}$ , preferably of from about  $1 \times 10^7$  to about  $1 \times 10^9$  plaque-forming units per kilogram. Preferably, viral vectors are administered parenterally; for example, in 3 doses, 4 weeks apart. It is preferable to avoid adding a chemical adjuvant to a composition containing a viral vector of the invention and

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thereby minimizing the immune response to the viral vector itself.

Non-toxicogenic *Vibrio cholerae* mutant strains that are useful as a live oral vaccine are known. Mekalanos et al.,  
5 Nature (1983) 306:551 and U.S. Patent No. 4,882,278 describe strains which have a substantial amount of the coding sequence of each of the two *ctxA* alleles deleted so that no functional *cholerae* toxin is produced. WO 92/11354 describes a strain in which the *irgA* locus is inactivated by mutation; this mutation  
10 can be combined in a single strain with *ctxA* mutations. WO 94/1533 describes a deletion mutant lacking functional *ctxA* and *attRS1* DNA sequences. These mutant strains are genetically engineered to express heterologous antigens, as described in WO 94/19482. An effective vaccine dose of a *Vibrio cholerae*  
15 strain capable of expressing a polypeptide or polypeptide derivative encoded by a DNA molecule of the invention contains about  $1 \times 10^5$  to about  $1 \times 10^9$ , preferably about  $1 \times 10^6$  to about  $1 \times 10^8$ , viable bacteria in a volume appropriate for the selected route of administration. Preferred routes of administration include  
20 all mucosal routes; most preferably, these vectors are administered intranasally or orally.

Attenuated *Salmonella typhimurium* strains, genetically engineered for recombinant expression of heterologous antigens or not, and their use as oral vaccines are described in  
25 Nakayama et al. (Bio/Technology (1988) 6:693) and WO 92/11361. Preferred routes of administration include all mucosal routes; most preferably, these vectors are administered intranasally or orally.

Other bacterial strains used as vaccine vectors in the  
30 context of the present invention are described in High et al., EMBO (1992) 11:1991 and Sizemore et al., Science (1995) 270:299 (*Shigella flexneri*); Medaglini et al., Proc. Natl. Acad. Sci. USA (1995) 92:6868 (*Streptococcus gordonii*), Flynn J.L., Cell.



Mol. Biol. (1994) 40 (suppl. I):31, WO 88/6626, WO 90/0594, WO 91/13157, WO 92/1796, and WO 92/21376 (Bacille Calmette Guérin).

In bacterial vectors, the polynucleotide of the invention is inserted into the bacterial genome or remains in a free state as part of a plasmid.

The composition comprising a vaccine bacterial vector of the present invention may further contain an adjuvant. A number of adjuvants are known to those skilled in the art. Preferred adjuvants are selected from the list provided below.

Accordingly, a fourth aspect of the invention provides (i) a composition of matter comprising a polynucleotide of the invention, together with a diluent or carrier; (ii) a pharmaceutical composition comprising a therapeutically or prophylactically effective amount of a polynucleotide of the invention; (iii) a method for inducing an immune response against *Chlamydia* in a mammal by administration of an immunogenically effective amount of a polynucleotide of the invention to elicit a protective immune response to *Chlamydia*; and particularly, (iv) a method for preventing and/or treating *Chlamydia* (e.g., *C. trachomatis*, *C. psittaci*, *C. pneumoniae*, or *C. pecorum*) infection, by administering a prophylactic or therapeutic amount of a polynucleotide of the invention to an infected individual. Additionally, the fourth aspect of the invention encompasses the use of a polynucleotide of the invention in the preparation of a medicament for preventing and/or treating *Chlamydia* infection. A preferred use includes the use of a DNA molecule placed under conditions for expression in a mammalian cell, especially in a plasmid that is unable to replicate in mammalian cells and to substantially integrate in a mammalian genome.

Use of the polynucleotides of the invention include their administration to a mammal as a vaccine, for therapeutic or prophylactic purposes. Such polynucleotides are used in the form of DNA as part of a plasmid that is unable to replicate in

a mammalian cell and unable to integrate into the mammalian genome. Typically, such a DNA molecule is placed under the control of a promoter suitable for expression in a mammalian cell. The promoter functions either ubiquitously or tissue-specifically. Examples of non-tissue specific promoters include the early Cytomegalovirus (CMV) promoter (described in U.S. Patent No. 4,168,062) and the Rous Sarcoma Virus promoter (described in Norton & Coffin, *Molec. Cell Biol.* (1985) 5:281). An example of a tissue-specific promoter is the desmin promoter which drives expression in muscle cells (Li *et al.*, *Gene* (1989) 78:243, Li & Paulin, *J. Biol. Chem.* (1991) 266:6562 and Li & Paulin, *J. Biol. Chem.* (1993) 268:10403). Use of promoters is well-known to those skilled in the art. Useful vectors are described in numerous publications, specifically WO 94/21797 and Hartikka *et al.*, *Human Gene Therapy* (1996) 7:1205.

Polynucleotides of the invention which are used as a vaccine encode either a precursor or a mature form of the corresponding polypeptide. In the precursor form, the signal peptide is either homologous or heterologous. In the latter case, a eucaryotic leader sequence such as the leader sequence of the tissue-type plasminogen factor (tPA) is preferred.

As used herein, a composition of the invention contains one or several polynucleotides with optionally at least one additional polynucleotide encoding another *Chlamydia* antigen such as urease subunit A, B, or both, or a fragment, derivative, mutant, or analog thereof. The composition may also contain an additional polynucleotide encoding a cytokine, such as interleukin-2 (IL-2) or interleukin-12 (IL-12) so that the immune response is enhanced. These additional polynucleotides are placed under appropriate control for expression. Advantageously, DNA molecules of the invention and/or additional DNA molecules to be included in the same composition, are present in the same plasmid.

Standard techniques of molecular biology for preparing and purifying polynucleotides are used in the preparation of polynucleotide therapeutics of the invention. For use as a vaccine, a polynucleotide of the invention is formulated according to various methods outlined below.

One method utilizes the polynucleotide in a naked form, free of any delivery vehicles. Such a polynucleotide is simply diluted in a physiologically acceptable solution such as sterile saline or sterile buffered saline, with or without a carrier. When present, the carrier preferably is isotonic, hypotonic, or weakly hypertonic, and has a relatively low ionic strength, such as provided by a sucrose solution, e.g., a solution containing 20% sucrose.

An alternative method utilizes the polynucleotide in association with agents that assist in cellular uptake. Examples of such agents are (i) chemicals that modify cellular permeability, such as bupivacaine (see, e.g., WO 94/16737), (ii) liposomes for encapsulation of the polynucleotide, or (iii) cationic lipids or silica, gold, or tungsten microparticles which associate themselves with the polynucleotides.

Anionic and neutral liposomes are well-known in the art (see, e.g., Liposomes: A Practical Approach, RPC New Ed, IRL press (1990), for a detailed description of methods for making liposomes) and are useful for delivering a large range of products, including polynucleotides. Cationic lipids are also known in the art and are commonly used for gene delivery. Such lipids include Lipofectin™ also known as DOTMA (N-[1-(2,3-dioleoyloxy)propyl]-N,N,N-trimethylammonium chloride), DOTAP (1,2-bis(oleoyloxy)-3-(trimethylammonio)propane), DDAB (dimethyldioctadecylammonium bromide), DOGS (dioctadecylamidologlycyl spermine) and cholesterol derivatives such as DC-Chol (3 beta-(N-(N',N'-dimethyl aminomethane)-carbamoyl) cholesterol). A description of these cationic lipids

can be found in EP 187,702, WO 90/11092, U.S. Patent No. 5,283,185, WO 91/15501, WO 95/26356, and U.S. Patent No. 5,527,928. Cationic lipids for gene delivery are preferably used in association with a neutral lipid such as DOPE (dioleyl 5 phosphatidylethanolamine), as described in WO 90/11092 as an example.

Formulation containing cationic liposomes may optionally contain other transfection-facilitating compounds. A number of them are described in WO 93/18759, WO 93/19768, WO 94/25608, and 10 WO 95/2397. They include spermine derivatives useful for facilitating the transport of DNA through the nuclear membrane (see, for example, WO 93/18759) and membrane-permeabilizing compounds such as GALA, Gramicidine S, and cationic bile salts (see, for example, WO 93/19768).

15 Gold or tungsten microparticles are used for gene delivery, as described in WO 91/359, WO 93/17706, and Tang et al. (Nature (1992) 356:152). The microparticle-coated polynucleotide is injected via intradermal or intraepidermal routes using a needleless injection device ("gene gun"), such as  
20 those described in U.S. Patent No. 4,945,050, U.S. Patent No. 5,015,580, and WO 94/24263.

The amount of DNA to be used in a vaccine recipient depends, e.g., on the strength of the promoter used in the DNA construct, the immunogenicity of the expressed gene product, the condition of the mammal intended for administration (e.g., the weight, age, and general health of the mammal), the mode of administration, and the type of formulation. In general, a therapeutically or prophylactically effective dose from about 1 µg to about 1 mg, preferably, from about 10 µg to about 800 µg and, more preferably, from about 25 µg to about 250 µg, can be administered to human adults. The administration can be achieved in a single dose or repeated at intervals.

The route of administration is any conventional route used in the vaccine field. As general guidance, a

polynucleotide of the invention is administered via a mucosal surface, e.g., an ocular, intranasal, pulmonary, oral, intestinal, rectal, vaginal, and urinary tract surface; or via a parenteral route, e.g., by an intravenous, subcutaneous, 5 intraperitoneal, intradermal, intraepidermal, or intramuscular route. The choice of administration route depends on the formulation that is selected. A polynucleotide formulated in association with bupivacaine is advantageously administered into muscles. When a neutral or anionic liposome or a cationic 10 lipid, such as DOTMA or DC-Chol, is used, the formulation can be advantageously injected via intravenous, intranasal (aerosolization), intramuscular, intradermal, and subcutaneous routes. A polynucleotide in a naked form can advantageously be administered via the intramuscular, intradermal, or sub- 15 cutaneous routes.

Although not absolutely required, such a composition can also contain an adjuvant. If so, a systemic adjuvant that does not require concomitant administration in order to exhibit an adjuvant effect is preferable such as, e.g., QS21, which is 20 described in U.S. Patent No. 5,057,546.

The sequence information provided in the present application enables the design of specific nucleotide probes and primers that are used for diagnostic purposes. Accordingly, a fifth aspect of the invention provides a nucleotide probe or 25 primer having a sequence found in or derived by degeneracy of the genetic code from a sequence shown in any one of SEQ ID Nos:1 to 26.

The term "probe" as used in the present application refers to DNA (preferably single stranded) or RNA molecules (or 30 modifications or combinations thereof) that hybridize under the stringent conditions, as defined above, to nucleic acid molecules having SEQ ID Nos: 1 to 26 or to sequences homologous to SEQ ID Nos:1 to 26, or to their complementary or anti-sense sequences. Generally, probes are significantly shorter than

full-length sequences . Such probes contain from about 5 to about 100, preferably from about 10 to about 80, nucleotides. In particular, probes have sequences that are at least 75%, preferably at least 85%, more preferably 95% homologous to a  
5 portion of any of SEQ ID Nos:1 to 26 or that are complementary to such sequences. Probes may contain modified bases such as inosine, methyl-5-deoxycytidine, deoxyuridine, dimethylamino-5-deoxyuridine, or diamino-2, 6-purine. Sugar or phosphate residues may also be modified or substituted. For example, a  
10 deoxyribose residue may be replaced by a polyamide (Nielsen et al., Science (1991) 254:1497) and phosphate residues may be replaced by ester groups such as diphosphate, alkyl, arylphosphonate and phosphorothioate esters. In addition, the 2'-hydroxyl group on ribonucleotides may be modified by  
15 including such groups as alkyl groups.

Probes of the invention are used in diagnostic tests, as capture or detection probes. Such capture probes are conventionally immobilized on a solid support, directly or indirectly, by covalent means or by passive adsorption. A  
20 detection probe is labelled by a detection marker selected from: radioactive isotopes, enzymes such as peroxidase, alkaline phosphatase, and enzymes able to hydrolyze a chromogenic, fluorogenic, or luminescent substrate, compounds that are chromogenic, fluorogenic, or luminescent, nucleotide base  
25 analogs, and biotin.

Probes of the invention are used in any conventional hybridization technique, such as dot blot (Maniatis et al., Molecular Cloning: A Laboratory Manual (1982) Cold Spring Harbor Laboratory Press, Cold Spring Harbor, New York), Southern blot  
30 (Southern, J. Mol. Biol. (1975) 98:503), northern blot (identical to Southern blot with the exception that RNA is used as a target), or the sandwich technique (Dunn et al., Cell (1977) 12:23). The latter technique involves the use of a specific capture probe and/or a specific detection probe with

nucleotide sequences that at least partially differ from each other.

A primer is a probe of usually about 10 to about 40 nucleotides that is used to initiate enzymatic polymerization of DNA in an amplification process (e.g., PCR), in an elongation process, or in a reverse transcription method. Primers used in diagnostic methods involving PCR are labeled by methods known in the art.

As described herein, the invention also encompasses (i) a reagent comprising a probe of the invention for detecting and/or identifying the presence of *Chlamydia* in a biological material; (ii) a method for detecting and/or identifying the presence of *Chlamydia* in a biological material, in which (a) a sample is recovered or derived from the biological material, (b) DNA or RNA is extracted from the material and denatured, and (c) exposed to a probe of the invention, for example, a capture, detection probe or both, under stringent hybridization conditions, such that hybridization is detected; and (iii) a method for detecting and/or identifying the presence of *Chlamydia* in a biological material, in which (a) a sample is recovered or derived from the biological material, (b) DNA is extracted therefrom, (c) the extracted DNA is primed with at least one, and preferably two, primers of the invention and amplified by polymerase chain reaction, and (d) the amplified DNA fragment is produced.

It is apparent that disclosure of polynucleotide sequences of SEQ ID Nos: 1 to 26, their homolog, and partial sequences of either enable their corresponding amino acid sequences. Accordingly, a sixth aspect of the invention features a substantially purified polypeptide or polypeptide derivative having an amino acid sequence encoded by a polynucleotide of the invention.

A "substantially purified polypeptide" as used herein is defined as a polypeptide that is separated from the environment

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in which it naturally occurs and/or that is free of the majority of the polypeptides that are present in the environment in which it was synthesized. For example, a substantially purified polypeptide is free from cytoplasmic polypeptides. Those  
5 skilled in the art would readily understand that the polypeptides of the invention may be purified from a natural source, i.e., a *Chlamydia* strain, or produced by recombinant means.

Consistent with the sixth aspect of the invention are  
10 polypeptides, homologs or fragments which are modified or treated to enhance their immunogenicity in the target animal, in whom the polypeptide, homolog or fragments are intended to confer protection against *Chlamydia*. Such modifications or treatments include: amino acid substitutions with an amino acid  
15 derivative such as 3-methylhistidine, 4-hydroxyproline, 5-hydroxylysine etc., modifications or deletions which are carried out after preparation of the polypeptide, homolog or fragment, such as the modification of free amino, carboxyl or hydroxyl side groups of the amino acids.

20 Identification of homologous polypeptides or polypeptide derivatives encoded by polynucleotides of the invention which have specific antigenicity is achieved by screening for cross-reactivity with an antiserum raised against the polypeptide of reference having an amino acid sequence of any one of SEQ ID  
25 Nos: 27 to 45. The procedure is as follows: a monospecific hyperimmune antiserum is raised against a purified reference polypeptide, a fusion polypeptide (for example, an expression product of MBP, GST, or His-tag systems), or a synthetic peptide predicted to be antigenic. Where an antiserum is raised  
30 against a fusion polypeptide, two different fusion systems are employed. Specific antigenicity can be determined according to a number of methods, including Western blot (Towbin et al., Proc. Natl. Acad. Sci. USA (1979) 76:4350), dot blot, and ELISA, as described below.



In a Western blot assay, the product to be screened, either as a purified preparation or a total *E. coli* extract, is submitted to SDS-Page electrophoresis as described by Laemmli (Nature (1970) 227:680). After transfer to a nitrocellulose membrane, the material is further incubated with the monospecific hyperimmune antiserum diluted in the range of dilutions from about 1:5 to about 1:5000, preferably from about 1:100 to about 1:500. Specific antigenicity is shown once a band corresponding to the product exhibits reactivity at any of the dilutions in the above range.

In an ELISA assay, the product to be screened is preferably used as the coating antigen. A purified preparation is preferred, although a whole cell extract can also be used. Briefly, about 100  $\mu$ l of a preparation at about 10  $\mu$ g protein/ml are distributed into wells of a 96-well polycarbonate ELISA plate. The plate is incubated for 2 hours at 37°C then overnight at 4°C. The plate is washed with phosphate buffer saline (PBS) containing 0.05% Tween 20 (PBS/Tween buffer). The wells are saturated with 250  $\mu$ l PBS containing 1% bovine serum albumin (BSA) to prevent non-specific antibody binding. After 1 hour incubation at 37°C, the plate is washed with PBS/Tween buffer. The antiserum is serially diluted in PBS/Tween buffer containing 0.5% BSA. 100  $\mu$ l of dilutions are added per well. The plate is incubated for 90 minutes at 37°C, washed and evaluated according to standard procedures. For example, a goat anti-rabbit peroxidase conjugate is added to the wells when specific antibodies were raised in rabbits. Incubation is carried out for 90 minutes at 37°C and the plate is washed. The reaction is developed with the appropriate substrate and the reaction is measured by colorimetry (absorbance measured spectrophotometrically). Under the above experimental conditions, a positive reaction is shown by O.D. values greater than a non immune control serum.

In a dot blot assay, a purified product is preferred, although a whole cell extract can also be used. Briefly, a solution of the product at about 100 µg/ml is serially two-fold diluted in 50 mM Tris-HCl (pH 7.5). 100 µl of each dilution are applied to a nitrocellulose membrane 0.45 µm set in a 96-well dot blot apparatus (Biorad). The buffer is removed by applying vacuum to the system. Wells are washed by addition of 50 mM Tris-HCl (pH 7.5) and the membrane is air-dried. The membrane is saturated in blocking buffer (50 mM Tris-HCl (pH 7.5) 0.15 M NaCl, 10 g/L skim milk) and incubated with an antiserum dilution from about 1:50 to about 1:5000, preferably about 1:500. The reaction is revealed according to standard procedures. For example, a goat anti-rabbit peroxidase conjugate is added to the wells when rabbit antibodies are used. Incubation is carried out 90 minutes at 37°C and the blot is washed. The reaction is developed with the appropriate substrate and stopped. The reaction is measured visually by the appearance of a colored spot, e.g., by colorimetry. Under the above experimental conditions, a positive reaction is shown once a colored spot is associated with a dilution of at least about 1:5, preferably of at least about 1:500.

Therapeutic or prophylactic efficacy of a polypeptide or derivative of the invention can be evaluated as described below. A seventh aspect of the invention provides (i) a composition of matter comprising a polypeptide of the invention together with a diluent or carrier; specifically (ii) a pharmaceutical composition containing a therapeutically or prophylactically effective amount of a polypeptide of the invention; (iii) a method for inducing an immune response against *Chlamydia* in a mammal, by administering to the mammal an immunogenically effective amount of a polypeptide of the invention to elicit a protective immune response to *Chlamydia*; and particularly, (iv) a method for preventing and/or treating a *Chlamydia* (e.g., *C. trachomatis*, *C. psittaci*, *C. pneumoniae*, or *C. pecorum*)

infection, by administering a prophylactic or therapeutic amount of a polypeptide of the invention to an infected individual. Additionally, the seventh aspect of the invention encompasses the use of a polypeptide of the invention in the preparation of  
5 a medicament for preventing and/or treating *Chlamydia* infection.

As used herein, the immunogenic compositions of the invention are administered by conventional routes known the vaccine field, in particular to a mucosal (e.g., ocular, intranasal, pulmonary, oral, gastric, intestinal, rectal,  
10 vaginal, or urinary tract) surface or via the parenteral (e.g., subcutaneous, intradermal, intramuscular, intravenous, or intraperitoneal) route. The choice of administration route depends upon a number of parameters, such as the adjuvant associated with the polypeptide. If a mucosal adjuvant is used,  
15 the intranasal or oral route is preferred. If a lipid formulation or an aluminum compound is used, the parenteral route is preferred with the sub-cutaneous or intramuscular route being most preferred. The choice also depends upon the nature of the vaccine agent. For example, a polypeptide of the  
20 invention fused to CTB or LTB is best administered to a mucosal surface.

As used herein, the composition of the invention contains one or several polypeptides or derivatives of the invention. The composition optionally contains at least one additional  
25 *Chlamydia* antigen, or a subunit, fragment, homolog, mutant, or derivative thereof.

For use in a composition of the invention, a polypeptide or derivative thereof is formulated into or with liposomes, preferably neutral or anionic liposomes, microspheres, ISCOMS,  
30 or virus-like-particles (VLPs) to facilitate delivery and/or enhance the immune response. These compounds are readily available to one skilled in the art; for example, see Liposomes: A Practical Approach (*supra*).

Adjuvants other than liposomes and the like are also used and are known in the art. Adjuvants may protect the antigen from rapid dispersal by sequestering it in a local deposit, or they may contain substances that stimulate the host to secrete 5 factors that are chemotactic for macrophages and other components of the immune system. An appropriate selection can conventionally be made by those skilled in the art, for example, from those described below.

Treatment is achieved in a single dose or repeated as 10 necessary at intervals, as can be determined readily by one skilled in the art. For example, a priming dose is followed by three booster doses at weekly or monthly intervals. An appropriate dose depends on various parameters including the recipient (e.g., adult or infant), the particular vaccine 15 antigen, the route and frequency of administration, the presence/absence or type of adjuvant, and the desired effect (e.g., protection and/or treatment), as can be determined by one skilled in the art. In general, a vaccine antigen of the invention is administered by a mucosal route in an amount from 20 about 10  $\mu$ g to about 500 mg, preferably from about 1 mg to about 200 mg. For the parenteral route of administration, the dose usually does not exceed about 1 mg, preferably about 100  $\mu$ g.

When used as vaccine agents, polynucleotides and polypeptides of the invention may be used sequentially as part 25 of a multistep immunization process. For example, a mammal is initially primed with a vaccine vector of the invention such as a pox virus, e.g., via the parenteral route, and then boosted twice with the polypeptide encoded by the vaccine vector, e.g., via the mucosal route. In another example, liposomes associated 30 with a polypeptide or derivative of the invention is also used for priming, with boosting being carried out mucosally using a soluble polypeptide or derivative of the invention in combination with a mucosal adjuvant (e.g., LT).

A polypeptide derivative of the invention is also used in accordance with the seventh aspect as a diagnostic reagent for detecting the presence of anti-*Chlamydia* antibodies, e.g., in a blood sample. Such polypeptides are about 5 to about 80, 5 preferably about 10 to about 50 amino acids in length. They are either labeled or unlabeled, depending upon the diagnostic method. Diagnostic methods involving such a reagent are described below.

Upon expression of a DNA molecule of the invention, a 10 polypeptide or polypeptide derivative is produced and purified using known laboratory techniques. As described above, the polypeptide or polypeptide derivative may be produced as a fusion protein containing a fused tail that facilitates purification. The fusion product is used to immunize a small 15 mammal, e.g., a mouse or a rabbit, in order to raise antibodies against the polypeptide or polypeptide derivative (monospecific antibodies). Accordingly, an eighth aspect of the invention provides a monospecific antibody that binds to a polypeptide or polypeptide derivative of the invention.

20 By "monospecific antibody" is meant an antibody that is capable of reacting with a unique naturally-occurring *Chlamydia* polypeptide. An antibody of the invention is either polyclonal or monoclonal. Monospecific antibodies may be recombinant, e.g., chimeric (e.g., constituted by a variable region of murine 25 origin associated with a human constant region), humanized (a human immunoglobulin constant backbone together with hypervariable region of animal, e.g., murine, origin), and/or single chain. Both polyclonal and monospecific antibodies may also be in the form of immunoglobulin fragments, e.g., F(ab)'2 30 or Fab fragments. The antibodies of the invention are of any isotype, e.g., IgG or IgA, and polyclonal antibodies are of a single isotype or a mixture of isotypes.

Antibodies against the polypeptides, homologs or fragments of the present invention are generated by immunization

of a mammal with a composition comprising said polypeptide, homolog or fragment. Such antibodies may be polyclonal or monoclonal. Methods to produce polyclonal or monoclonal antibodies are well known in the art. For a review, see

- 5 "Antibodies, A Laboratory Manual, Cold Spring Harbor Laboratory, Eds. E. Harlow and D. Lane (1988), and D.E. Yelton et al., 1981. Ann. Rev. Biochem. 50:657-680. For monoclonal antibodies, see Kohl and Milstein?...

The antibodies of the invention, which are raised to a  
10 polypeptide or polypeptide derivative of the invention, are produced and identified using standard immunological assays, e.g., Western blot analysis, dot blot assay, or ELISA (see, e.g., Coligan et al., Current Protocols in Immunology (1994) John Wiley & Sons, Inc., New York, NY). The antibodies are used  
15 in diagnostic methods to detect the presence of a *Chlamydia* antigen in a sample, such as a biological sample. The antibodies are also used in affinity chromatography for purifying a polypeptide or polypeptide derivative of the invention. As is discussed further below, such antibodies may  
20 be used in prophylactic and therapeutic passive immunization methods.

Accordingly, a ninth aspect of the invention provides  
(i) a reagent for detecting the presence of *Chlamydia* in a biological sample that contains an antibody, polypeptide, or  
25 polypeptide derivative of the invention; and (ii) a diagnostic method for detecting the presence of *Chlamydia* in a biological sample, by contacting the biological sample with an antibody, a polypeptide, or a polypeptide derivative of the invention, such that an immune complex is formed, and by detecting such complex  
30 to indicate the presence of *Chlamydia* in the sample or the organism from which the sample is derived.

Those skilled in the art will readily understand that the immune complex is formed between a component of the sample and the antibody, polypeptide, or polypeptide derivative, whichever

is used, and that any unbound material is removed prior to detecting the complex. It is understood that a polypeptide reagent is useful for detecting the presence of anti-*Chlamydia* antibodies in a sample, e.g., a blood sample, while an antibody of the invention is used for screening a sample, such as a gastric extract or biopsy, for the presence of *Chlamydia* polypeptides.

For diagnostic applications, the reagent (i.e., the antibody, polypeptide, or polypeptide derivative of the invention) is either in a free state or immobilized on a solid support, such as a tube, a bead, or any other conventional support used in the field. Immobilization is achieved using direct or indirect means. Direct means include passive adsorption (non-covalent binding) or covalent binding between the support and the reagent. By "indirect means" is meant that an anti-reagent compound that interacts with a reagent is first attached to the solid support. For example, if a polypeptide reagent is used, an antibody that binds to it can serve as an anti-reagent, provided that it binds to an epitope that is not involved in the recognition of antibodies in biological samples. Indirect means may also employ a ligand-receptor system, for example, where a molecule such as a vitamin is grafted onto the polypeptide reagent and the corresponding receptor immobilized on the solid phase. This is illustrated by the biotin-streptavidin system. Alternatively, a peptide tail is added chemically or by genetic engineering to the reagent and the grafted or fused product immobilized by passive adsorption or covalent linkage of the peptide tail.

Such diagnostic agents may be included in a kit which also comprises instructions for use. The reagent are labeled with a detection means which allows for the detection of the reagent when it is bound to its target. The detection means may be a fluorescent agent such as fluorescein isocyanate or fluorescein isothiocyanate, or an enzyme such as horse radish

peroxidase or luciferase or alkaline phosphatase, or a radioactive element such as  $^{125}\text{I}$  or  $^{51}\text{Cr}$ .

Accordingly, a tenth aspect of the invention provides a process for purifying, from a biological sample, a polypeptide  
5 or polypeptide derivative of the invention, which involves carrying out antibody-based affinity chromatography with the biological sample, wherein the antibody is a monospecific antibody of the invention.

For use in a purification process of the invention, the  
10 antibody is either polyclonal or monospecific, and preferably is of the IgG type. Purified IgGs is prepared from an antiserum using standard methods (see, e.g., Coligan et al., supra). Conventional chromatography supports, as well as standard methods for grafting antibodies, are described in, e.g.,  
15 Antibodies: A Laboratory Manual, D. Lane, E. Harlow, Eds. (1988) and outlined below.

Briefly, a biological sample, such as an *C. pneumoniae* extract preferably in a buffer solution, is applied to a chromatography material, preferably equilibrated with the buffer  
20 used to dilute the biological sample so that the polypeptide or polypeptide derivative of the invention (i.e., the antigen) is allowed to adsorb onto the material. The chromatography material, such as a gel or a resin coupled to an antibody of the invention, is in either a batch form or a column. The unbound  
25 components are washed off and the antigen is then eluted with an appropriate elution buffer, such as a glycine buffer or a buffer containing a chaotropic agent, e.g., guanidine HCl, or high salt concentration (e.g., 3 M  $\text{MgCl}_2$ ). Eluted fractions are recovered and the presence of the antigen is detected, e.g., by measuring  
30 the absorbance at 280 nm.

An eleventh aspect of the invention provides (i) a composition of matter comprising a monospecific antibody of the invention, together with a diluent or carrier; (ii) a pharmaceutical composition comprising a therapeutically or



prophylactically effective amount of a monospecific antibody of the invention, and (iii) a method for treating or preventing a *Chlamydia* (e.g., *C. trachomatis*, *C. psittaci*, *C. pneumoniae* or *C. pecorum*) infection, by administering a therapeutic or  
5 prophylactic amount of a monospecific antibody of the invention to an infected individual. Additionally, the eleventh aspect of the invention encompasses the use of a monospecific antibody of the invention in the preparation of a medicament for treating or preventing *Chlamydia* infection.

10 The monospecific antibody is either polyclonal or monoclonal, preferably of the IgA isotype (predominantly). In passive immunization, the antibody is administered to a mucosal surface of a mammal, e.g., the gastric mucosa, e.g., orally or intragastrically, advantageously, in the presence of a  
15 bicarbonate buffer. Alternatively, systemic administration, not requiring a bicarbonate buffer, is carried out. A monospecific antibody of the invention is administered as a single active component or as a mixture with at least one monospecific antibody specific for a different *Chlamydia* polypeptide. The  
20 amount of antibody and the particular regimen used are readily determined by one skilled in the art. For example, daily administration of about 100 to 1,000 mg of antibodies over one week, or three doses per day of about 100 to 1,000 mg of antibodies over two or three days, are effective regimens for  
25 most purposes.

Therapeutic or prophylactic efficacy are evaluated using standard methods in the art, e.g., by measuring induction of a mucosal immune response or induction of protective and/or therapeutic immunity, using, e.g., the *C. pneumoniae* mouse  
30 model. Those skilled in the art will readily recognize that the *C. pneumoniae* strain of the model may be replaced with another *Chlamydia* strain. For example, the efficacy of DNA molecules and polypeptides from *C. pneumoniae* is preferably evaluated in a mouse model using *C. pneumoniae* strain. Protection is

determined by comparing the degree of *Chlamydia* infection to that of a control group. Protection is shown when infection is reduced by comparison to the control group. Such an evaluation is made for polynucleotides, vaccine vectors, polypeptides and derivatives thereof, as well as antibodies of the invention.

Adjuvants useful in any of the vaccine compositions described above are as follows.

Adjuvants for parenteral administration include aluminum compounds, such as aluminum hydroxide, aluminum phosphate, and aluminum hydroxy phosphate. The antigen is precipitated with, or adsorbed onto, the aluminum compound according to standard protocols. Other adjuvants, such as RIBI (ImmunoChem, Hamilton, MT), is used in parenteral administration.

Adjuvants for mucosal administration include bacterial toxins, e.g., the cholera toxin (CT), the *E. coli* heat-labile toxin (LT), the *Clostridium difficile* toxin A and the pertussis toxin (PT), or combinations, subunits, toxoids, or mutants thereof such as a purified preparation of native cholera toxin subunit B (CTB). Fragments, homologs, derivatives, and fusions to any of these toxins are also suitable, provided that they retain adjuvant activity. Preferably, a mutant having reduced toxicity is used. Suitable mutants are described, e.g., in WO 95/17211 (Arg-7-Lys CT mutant), WO 96/6627 (Arg-192-Gly LT mutant), and WO 95/34323 (Arg-9-Lys and Glu-129-Gly PT mutant). Additional LT mutants that are used in the methods and compositions of the invention include, e.g., Ser-63-Lys, Ala-69-Gly, Glu-110-Asp, and Glu-112-Asp mutants. Other adjuvants, such as a bacterial monophosphoryl lipid A (MPLA) of, e.g., *E. coli*, *Salmonella minnesota*, *Salmonella typhimurium*, or *Shigella flexneri*; saponins, or polylactide glycolide (PLGA) microspheres, is also be used in mucosal administration.

Adjuvants useful for both mucosal and parenteral administrations include polyphosphazene (WO 95/2415), DC-chol (3

b-(N-(N',N'-dimethyl aminomethane)-carbamoyl) cholesterol; U.S. Patent No. 5,283,185 and WO 96/14831) and QS-21 (WO 88/9336).

Any pharmaceutical composition of the invention containing a polynucleotide, a polypeptide, a polypeptide  
5 derivative, or an antibody of the invention, is manufactured in a conventional manner. In particular, it is formulated with a pharmaceutically acceptable diluent or carrier, e.g., water or a saline solution such as phosphate buffer saline. In general, a diluent or carrier is selected on the basis of the mode and  
10 route of administration, and standard pharmaceutical practice. Suitable pharmaceutical carriers or diluents, as well as pharmaceutical necessities for their use in pharmaceutical formulations, are described in *Remington's Pharmaceutical Sciences*, a standard reference text in this field and in the  
15 USP/NF.

The invention also includes methods in which *Chlamydia* infection are treated by oral administration of a *Chlamydia* polypeptide of the invention and a mucosal adjuvant, in combination with an antibiotic, an antacid, sucralfate, or a  
20 combination thereof. Examples of such compounds that can be administered with the vaccine antigen and the adjuvant are antibiotics, including, e.g., macrolides, tetracyclines, and derivatives thereof (specific examples of antibiotics that can be used include azithromycin or doxycyclin or immunomodulators  
25 such as cytokines or steroids). In addition, compounds containing more than one of the above-listed components coupled together, are used. The invention also includes compositions for carrying out these methods, i.e., compositions containing a *Chlamydia* antigen (or antigens) of the invention, an adjuvant,  
30 and one or more of the above-listed compounds, in a pharmaceutically acceptable carrier or diluent.

Amounts of the above-listed compounds used in the methods and compositions of the invention are readily determined by one skilled in the art. Treatment/immunization schedules are also

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known and readily designed by one skilled in the art. For example, the non-vaccine components can be administered on days 1-14, and the vaccine antigen + adjuvant can be administered on days 7, 14, 21, and 28.

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CLAIMS:

1. A nucleic acid molecule comprising a nucleic acid sequence which encodes a polypeptide selected from any of:

(a) SEO ID Nos: 27 to 45;

5 (b) an immunogenic fragment comprising at least 12  
consecutive amino acids from a polypeptide of (a); and

(c) a polypeptide of (a) or (b) which has been modified without loss of immunogenicity, wherein said modified polypeptide is at least 75% identical in amino acid sequence to the corresponding polypeptide of (a) or (b).

2. A nucleic acid molecule comprising a nucleic acid sequence selected from any of:

(a) SEQ ID Nos: 1 to 26;

(b) a sequence which encodes a polypeptide encoded by  
15 any one of SEQ ID Nos: 1 to 26;

(c) a sequence comprising at least 38 consecutive nucleotides from any one of the nucleic acid sequences of (a) and (b); and

(d) a sequence which encodes a polypeptide which is  
20 at least 75% identical in amino acid sequence to any one of the  
polypeptides encoded by SEQ ID Nos: 1 to 26.

3. A nucleic acid molecule comprising a nucleic acid sequence which is anti-sense to the nucleic acid molecule of claim 1.

25 4. A nucleic acid molecule comprising a nucleic acid sequence which encodes a fusion protein, said fusion protein comprising a polypeptide encoded by a nucleic acid molecule according to claim 1 and a second polypeptide.



5. The nucleic acid molecule of claim 4 wherein the second polypeptide is a heterologous signal peptide.

6. The nucleic acid molecule of claim 4 wherein the second polypeptide has adjuvant activity.

7. A nucleic acid molecule according to claim 1, operatively linked to one or more expression control sequences.

8. A vaccine comprising a vaccine vector and at least one first nucleic acid selected from any of:

(i) SEQ ID Nos: 1 to 26;

(ii) a nucleic acid sequence which encodes a polypeptide encoded by any one of SEQ ID Nos: 1 to 26;

(iii) a nucleic acid sequence comprising at least 38 consecutive nucleotides from any one of the nucleic acid sequences of (i) and (ii);

(iv) a nucleic acid sequence which encodes a polypeptide which is at least 75% identical in amino acid sequence to the polypeptide encoded by any one of SEQ ID Nos: 1 to 26;

(v) a nucleic acid sequence which encodes a polypeptide whose sequence is set forth in any one of SEQ ID Nos: 27 to 45;

(vi) a nucleic acid sequence which encodes an immunogenic fragment comprising at least 12 consecutive amino acids from any one of SEQ ID Nos: 27 to 45; and

(vii) a nucleic acid sequence which encodes a polypeptide as defined in (v) or an immunogenic fragment as defined in (vi) which has been modified without loss of immunogenicity, wherein said modified polypeptide or fragment is at least 75% identical in amino acid sequence to the

corresponding polypeptide of (v) or the corresponding fragment of (vi);

wherein each first nucleic acid is capable of being expressed.

- 5 9. A vaccine comprising a vaccine vector and at least one first nucleic acid encoding a fusion protein, wherein the fusion protein comprises:

(a) a first polypeptide selected from any of:

10 (i) a polypeptide encoded by any one of SEQ ID Nos: 1 to 26;

(ii) a polypeptide encoded by a nucleic acid sequence comprising at least 38 consecutive nucleotides from any one of SEQ ID Nos: 1 to 26;

15 (iii) a polypeptide which is at least 75% identical in amino acid sequence to the polypeptide encoded by any one of SEQ ID Nos: 1 to 26;

(iv) a polypeptide whose sequence is set forth in any one of SEQ ID Nos: 27 to 45;

20 (v) an immunogenic fragment comprising at least 12 consecutive amino acids from any one of SEQ ID Nos: 27 to 45; and

(vi) a polypeptide as defined (iv) or an immunogenic fragment as defined in (v) which has been modified without loss of immunogenicity, wherein said modified polypeptide or  
25 fragment is at least 75% identical in amino acid sequence to the corresponding polypeptide of (iv) or the corresponding fragment of (v); and

(b) a second polypeptide;

wherein each first nucleic acid is capable of being expressed.

10. The vaccine of claim 9 wherein the second polypeptide is a heterologous signal peptide.

5 11. The vaccine of claim 9 wherein the second polypeptide has adjuvant activity.

12. The vaccine of claim 8 wherein each first nucleic acid is operatively linked to one or more expression control sequences.

10 13. A vaccine according to claim 8 wherein each first nucleic acid is expressed as a polypeptide, and wherein the vaccine comprises a second nucleic acid encoding an additional polypeptide which enhances the immune response to the polypeptide expressed by the first nucleic acid.

15 14. The vaccine of claim 13 wherein the second nucleic acid encodes an additional *Chlamydia* polypeptide.

15. A pharmaceutical composition comprising a nucleic acid according to claim 1 and a pharmaceutically acceptable carrier.

20 16. A pharmaceutical composition comprising a vaccine according to claim 8 and a pharmaceutically acceptable carrier.

17. A unicellular host transformed with the nucleic acid molecule of claim 7.

18. An isolated nucleic acid probe of 5 to 100  
25 nucleotides which hybridizes under stringent conditions to any one of nucleic acid molecules of SEQ ID Nos: 1 to 26, or to a complementary or anti-sense sequence of said nucleic acid molecule.

19. A primer of 10 to 40 nucleotides which hybridizes  
30 under stringent conditions to any one of nucleic acid molecules

of SEQ ID Nos: 1 to 26, or to a homolog or complementary or anti-sense sequence of said nucleic acid molecule.

20. A polypeptide encoded by a nucleic acid sequence according to claim 2.

5 21. A polypeptide comprising an amino acid sequence selected from any of:

(a) SEQ ID Nos: 27 to 45;

(b) an immunogenic fragment comprising at least 12 consecutive amino acids from a polypeptide of (a); and

10 (c) a polypeptide of (a) or (b) which has been modified without loss of immunogenicity, wherein said modified polypeptide is at least 75% identical in amino acid sequence to the corresponding polypeptide of (a) or (b).

22. A fusion protein comprising a polypeptide of claim 20  
15 and a second polypeptide.

23. The fusion protein of claim 22 wherein the second polypeptide is a heterologous signal peptide.

24. The fusion protein of claim 22 wherein the second polypeptide has adjuvant activity.

20 25. A method for producing a polypeptide of claim 20, comprising the step of culturing a unicellular host of claim 17.

26. An antibody against the polypeptide of claim 20.

27. A vaccine comprising at least one first polypeptide  
25 selected from any of:

(i) a polypeptide encoded by any one of SEQ ID Nos: 1 to 26;

(ii) a polypeptide encoded by a nucleic acid sequence comprising at least 38 consecutive nucleotides from any one of SEQ ID Nos: 1 to 26;

5 (iii) a polypeptide which is at least 75% identical in amino acid sequence to the polypeptide encoded by any one of SEQ ID Nos: 1 to 26;

(iv) a polypeptide whose sequence is set forth in any one of SEQ ID Nos: 27 to 45;

10 (v) an immunogenic fragment comprising at least 12 consecutive amino acids from any one of SEQ ID Nos: 27 to 45; and

(vi) a polypeptide as defined in (iv) or an immunogenic fragment as defined in (v) which has been modified without loss of immunogenicity, wherein said modified  
15 polypeptide or fragment is at least 75% identical in amino acid sequence to the corresponding polypeptide of (iv) or the corresponding fragment of (v).

28. A vaccine comprising at least one fusion protein, wherein the fusion protein comprises:

20 (a) a first polypeptide selected from any of:

(i) a polypeptide encoded by any one of SEQ ID Nos: 1 to 26;

(ii) a polypeptide encoded by a nucleic acid sequence comprising at least 38 consecutive nucleotides from any one of  
25 SEQ ID Nos: 1 to 26;

(iii) a polypeptide which is at least 75% identical in amino acid sequence to the polypeptide encoded by any one of SEQ ID Nos: 1 to 26;

(iv) a polypeptide whose sequence is set forth in any  
30 one of SEQ ID Nos: 27 to 45;

(v) an immunogenic fragment comprising at least 12 consecutive amino acids from any one of SEQ ID Nos: 27 to 45; and

5 (vi) a polypeptide as defined (iv) or an immunogenic fragment as defined in (v) which has been modified without loss of immunogenicity, wherein said modified polypeptide or fragment is at least 75% identical in amino acid sequence to the corresponding polypeptide of (iv) or the corresponding fragment of (v); and

10 (b) a second polypeptide.

29. The vaccine of claim 28 wherein the second polypeptide is a heterologous signal peptide.

30. The vaccine of claim 28 wherein the second polypeptide has adjuvant activity.

15 31. A vaccine comprising at least one first polypeptide according to claim 20 and an additional polypeptide which enhances the immune response to the first polypeptide.

32. The vaccine of claim 31 wherein the additional polypeptide comprises a *Chlamydia* polypeptide.

20 33. A pharmaceutical composition comprising a polypeptide according to claim 20 and a pharmaceutically acceptable carrier.

34. A pharmaceutical composition comprising a vaccine according to claim 27 and a pharmaceutically acceptable  
25 carrier.

35. A pharmaceutical composition comprising an antibody according to claim 26 and a pharmaceutically acceptable carrier.

36. A method for preventing or treating *Chlamydia* infection comprising administering to a patient an effective amount of:

(a) a nucleic acid molecule according to claim 2;

5 (b) a vaccine comprising a vaccine vector and at least one first nucleic acid according to claim 2;

(c) a pharmaceutical composition comprising a nucleic acid according to claim 2 and a pharmaceutically acceptable carrier;

10 (d) a polypeptide encoded by a nucleic acid sequence according to claim 2; or

(e) an antibody against a polypeptide encoded by a nucleic acid sequence according to claim 2.

37. A method of detecting *Chlamydia* infection comprising  
15 the step of contacting a body fluid of a mammal to be tested, with a component selected from any one of:

(a) a nucleic acid molecule according to claim 2;

(b) a polypeptide encoded by a nucleic acid sequence according to claim 2; and

20 (c) an antibody against a polypeptide encoded by a nucleic acid sequence according to claim 2.

38. A diagnostic kit comprising instructions for use and a component selected from any one of:

(a) a nucleic acid molecule according to claim 2;

25 (b) a polypeptide encoded by a nucleic acid sequence according to claim 2; and

(c) an antibody against a polypeptide encoded by a nucleic acid sequence according to claim 2.

39. A method for identifying a polypeptide of claim 20 which induces an immune response effective to prevent or lessen the severity of *Chlamydia* infection in a mammal previously immunized with polypeptide, comprising the steps of:

5 (a) immunizing a mouse with a polypeptide of claim 20; and

(b) inoculating the immunized mouse with *Chlamydia*;

wherein the polypeptide which prevents or lessens the severity of *Chlamydia* infection in the immunized mouse compared  
10 to a non-immunized control mouse is identified.



CLAIMS

1. A nucleic acid molecule comprising a nucleic acid  
sequence which encodes a polypeptide selected from any of:
- 5 (a) SEQ ID Nos: 27 to 45;
- (b) an immunogenic fragment comprising at least 12  
consecutive amino acids from a polypeptide of (a); and
- (c) a polypeptide of (a) or (b) which has been modified to  
improve its immunogenicity, wherein said modified  
10 polypeptide is at least 75% identical in amino acid  
sequence to the corresponding polypeptide of (a) or  
(b).
2. A nucleic acid molecule comprising a nucleic acid  
15 sequence selected from any of:
- (a) SEQ ID Nos: 1 to 26;
- (b) a sequence which encodes a polypeptide encoded by any  
one of SEQ ID Nos: 1 to 26;
- (c) a sequence comprising at least 38 consecutive  
20 nucleotides from any one of the nucleic acid sequences  
of (a) and (b); and
- (d) a sequence which encodes a polypeptide which is at  
least 75% identical in amino acid sequence to any one  
of the polypeptides encoded by SEQ ID Nos: 1 to 26.

3. A nucleic acid molecule comprising a nucleic acid sequence which encodes a fusion protein, said fusion protein comprising a polypeptide encoded by a nucleic acid molecule according to claim 1 and an additional polypeptide.
- 5
4. A nucleic acid molecule according to claim 1, operatively linked to one or more expression control sequences.
- 10
5. A vaccine comprising at least one first nucleic acid according to any one of claims 1 to 4 and a vaccine vector wherein each first nucleic acid is expressed as a polypeptide, the vaccine optionally comprising a second nucleic acid encoding an additional polypeptide which enhances the immune response to the polypeptide expressed by said first nucleic acid.
- 15
6. The vaccine of claim 5 wherein the second nucleic acid encodes an additional *Chlamydia* polypeptide.
- 20
7. A pharmaceutical composition comprising a nucleic acid according to any one of claims 1 to 5 and a pharmaceutically acceptable carrier.
- 25

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8. A pharmaceutical composition comprising a vaccine according to claim 5 or 6 and a pharmaceutically acceptable carrier.
- 5 9. A unicellular host transformed with the nucleic acid molecule of claim 4.
10. A nucleic acid probe of 5 to 100 nucleotides which hybridizes under stringent conditions to any one of nucleic acid molecules of SEQ ID Nos: 1 to 26, or to a homolog or complementary or anti-sense sequence of said nucleic acid molecule.
- 10 11. A primer of 10 to 40 nucleotides which hybridizes under stringent conditions to any one of nucleic acid molecules of SEQ ID Nos: 1 to 26, or to a homolog or complementary or anti-sense sequence of said nucleic acid molecule.
- 15 12. A polypeptide encoded by a nucleic acid sequence according to any one of claims 1 to 4.
- 20 13. A polypeptide comprising an amino acid sequence selected from any of:
- 25 (a) SEQ ID Nos: 27 to 45;

- (b) an immunogenic fragment comprising at least 12 consecutive amino acids from a polypeptide of (a); and
- (c) a polypeptide of (a) or (b) which has been modified to improve its immunogenicity, wherein said modified polypeptide is at least 75% identical in amino acid sequence to the corresponding polypeptide of (a) or (b).
14. A fusion polypeptide comprising a polypeptide of claim 12 or 13 and an additional polypeptide.
15. A method for producing a polypeptide of claim 12 or 13, comprising the step of culturing a unicellular host according to claim 9.
16. An antibody against the polypeptide of any one of claims 12 to 14.
17. A vaccine comprising at least one first polypeptide according to any one of claims 12 to 14 and a pharmaceutically acceptable carrier, optionally comprising a second polypeptide which enhances the immune response to the first polypeptide.
18. The vaccine of claim 17 wherein the second polypeptide comprises an additional *Chlamydia* polypeptide.

19. A pharmaceutical composition comprising a polypeptide according to any one of claims 12 to 14 and a pharmaceutically acceptable carrier.

5

20. A pharmaceutical composition comprising a vaccine according to claim 17 or 18 and a pharmaceutically acceptable carrier.

- 10 21. A pharmaceutical composition comprising an antibody according to claim 16 and a pharmaceutically acceptable carrier.

22. A method for preventing or treating *Chlamydia*  
15 infection using:  
(a) the nucleic acid of any one of claims 1 to 4;  
(b) the vaccine of any one of claims 5, 6, 17 and 18;  
(c) the pharmaceutical composition of any one of claims 7, 8, 19 to 21;  
20 (d) the polypeptide of any one of claims 12 to 14; or  
(e) the antibody of claim 16.

23. A method of detecting *Chlamydia* infection comprising the step of assaying a body fluid of a mammal to be tested,  
25 with a component selected from any one of:  
(a) the nucleic acid of any one of claims 1 to 4;



CORRECTED VERSION

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1/68, C12N 5/10[CA/CA]: 51 Aspenwood Drive, Toronto, Ontario M2H  
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60/106,074	29 October 1998 (29.10.1998)	US
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60/107,035	2 November 1998 (02.11.1998)	US
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(54) Title: CHLAMYDIA ANTIGENS AND CORRESPONDING DNA FRAGMENTS AND USES THEREOF

(57) Abstract: The present invention provides purified and isolated polynucleotide molecules that encode *Chlamydia* polypeptides which can be used in methods to prevent, treat, and diagnose *Chlamydia* infection. In one form of the invention, the polynucleotide molecules are selected from DNA that encode polypeptides CPN100397 (SEQ ID Nos: 1 and 2), CPN100421 (SEQ ID Nos: 3 and 4), CPN100422 (SEQ ID Nos: 4 and 6), CPN100424 (SEQ ID Nos: 7 and 8), CPN100426 (SEQ ID Nos: 9 and 10), CPN100508 (SEQ ID Nos: 11 and 12), CPN100515 (SEQ ID Nos: 13 and 14), CPN100538 (SEQ ID Nos: 15 and 16), CPN100557 (SEQ ID Nos: 17 and 18), CPN100622 (SEQ ID Nos: 19 and 20), CPN100626 (SEQ ID Nos: 21 and 22), CPN100628 (SEQ ID Nos: 23 and 24) and CPN100630 (SEQ ID Nos: 25 and 26).

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Title: CHLAMYDIA ANTIGENS AND  
CORRESPONDING DNA FRAGMENTS  
AND USES THEREOF

Inventor(s): Andrew D. MURDIN et al  
DOCKET NO.: 032931/0251

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Figure 1: CPN100397

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attttaacgt gcgtatcatt tgtgactaag agatagacct gctttcttta tctatcttct 60
gtattggaaa gaaagccctt tgagggaataa aaaggttggt atg aag att cca ctc 115
                                         Met Lys Ile Pro Leu
                                         1 5
cgc ttt tta ttg ata tca tta gta cct acg ctt tct atg tcg aat tta 163
Arg Phe Leu Leu Ile Ser Leu Val Pro Thr Leu Ser Met Ser Asn Leu
10 15 20
tta gga gct gct act acc gaa gag tta tcg gct agc aat agc ttc gat 211
Leu Gly Ala Ala Thr Thr Glu Glu Leu Ser Ala Ser Asn Ser Phe Asp
25 30 35
gga act aca tca aca aca agc ttt tct agt aaa aca tca tcg gct aca 259
Gly Thr Thr Ser Thr Thr Ser Phe Ser Ser Lys Thr Ser Ser Ala Thr
40 45 50
gat ggc acc aat tat gtt ttt aaa gat tct gta gtt ata gaa aat gta 307
Asp Gly Thr Asn Tyr Val Phe Lys Asp Ser Val Val Ile Glu Asn Val
55 60 65
ccc aaa aca ggg gaa act cag tct act agt tgt ttt aaa aat gac gct 355
Pro Lys Thr Gly Glu Thr Gln Ser Thr Ser Cys Phe Lys Asn Asp Ala
70 75 80 85
gca gct gga gat cta aat ttc tta gga ggg gga ttt tct ttc aca ttt 403
Ala Ala Gly Asp Leu Asn Phe Leu Gly Gly Gly Phe Ser Phe Thr Phe
90 95 100
agc aat atc gat gca acc acg gct tct gga gct gct att gga agt gaa 451
Ser Asn Ile Asp Ala Thr Thr Ala Ser Gly Ala Ala Ile Gly Ser Glu
105 110 115
gca gct aat aag aca gtc acg tta tca gga ttt tcg gca ctt tct ttt 499
Ala Ala Asn Lys Thr Val Thr Leu Ser Gly Phe Ser Ala Leu Ser Phe
120 125 130
ctt aaa tcc cca gca agt aca gtg act aat gga ttg gga gct atc aat 547
Leu Lys Ser Pro Ala Ser Thr Val Thr Asn Gly Leu Gly Ala Ile Asn
135 140 145
gtt aaa ggg aat tta agc cta ttg gat aat gat aag gta ttg att cag 595
Val Lys Gly Asn Leu Ser Leu Leu Asp Asn Lys Val Leu Ile Gln
150 155 160 165
gac aat ttc tca aca gga gat ggc gga gca att aat tgt gca ggc tcc 643
Asp Asn Phe Ser Thr Gly Asp Gly Gly Ala Ile Asn Cys Ala Gly Ser
170 175 180
ttg aag atc gca aac aat aag tcc ctt tct ttt att gga aat agt tct 691
Leu Lys Ile Ala Asn Asn Lys Ser Leu Ser Phe Ile Gly Asn Ser Ser
185 190 195

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Fig. 1 (con't)

tca aca cgt ggc gga gcg att cat acc aaa aac ctc aca cta tct tct	739
Ser Thr Arg Gly Gly Ala Ile His Thr Lys Asn Leu Thr Leu Ser Ser	
200 205 210	
ggt ggg gaa act cta ttt cag ggg aat aca gcg cct acg gct gct ggt	787
Gly Gly Glu Thr Leu Phe Gln Gly Asn Thr Ala Pro Thr Ala Ala Gly	
215 220 225	
aaa gga ggt gct atc gcg att gca gac tct ggc acc cta tcc att tct	835
Lys Gly Gly Ala Ile Ala Ile Ala Asp Ser Gly Thr Leu Ser Ile Ser	
230 235 240 245	
gga gac agt ggc gac att atc ttt gaa ggc aat acg ata gga gct aca	883
Gly Asp Ser Gly Asp Ile Ile Phe Glu Gly Asn Thr Ile Gly Ala Thr	
250 255 260	
gga acc gtc tct cat agt gct att gat tta gga act agc gct aag ata	931
Gly Thr Val Ser His Ser Ala Ile Asp Leu Gly Thr Ser Ala Lys Ile	
265 270 275	
act gcg tta cgt gct gcg caa gga cat acg ata tac ttt tat gat cgg	979
Thr Ala Leu Arg Ala Ala Gln Gly His Thr Ile Tyr Phe Tyr Asp Pro	
280 285 290	
att act gta aca gga tcg aca tct gtt gct gat gct ctc aat att aat	1027
Ile Thr Val Thr Gly Ser Thr Ser Val Ala Asp Ala Leu Asn Ile Asn	
295 300 305	
agc cct gat act gga gat aac aaa gag tat acg gga acc ata gtc ttt	1075
Ser Pro Asp Thr Gly Asp Asn Lys Glu Tyr Thr Gly Thr Ile Val Phe	
310 315 320 325	
tct gga gag aag ctc acg gag gca gaa gct aaa gat gag aag aac cgc	1123
Ser Gly Glu Lys Leu Thr Glu Ala Glu Ala Lys Asp Glu Lys Asn Arg	
330 335 340	
act tct aaa tta ctt caa aat gtt gct ttt aaa aat ggg act gta gtt	1171
Thr Ser Lys Leu Leu Gln Asn Val Ala Phe Lys Asn Gly Thr Val Val	
345 350 355	
tta aaa ggt gat gtc gtt tta agt gcg aac ggt ttc tct cag gat gca	1219
Leu Lys Gly Asp Val Val Leu Ser Ala Asn Gly Phe Ser Gln Asp Ala	
360 365 370	
aac tct aag ttg att atg gat tta ggg acg tcg ttg gtt gca aac acc	1267
Asn Ser Lys Leu Ile Met Asp Leu Gly Thr Ser Leu Val Ala Asn Thr	
375 380 385	
gaa agt atc gag tta acg aat ttg gaa att aat ata gac tct ctc agg	1315
Glu Ser Ile Glu Leu Thr Asn Leu Glu Ile Asn Ile Asp Ser Leu Arg	
390 395 400 405	

Fig. 1 (con't)

aac ggg aaa aag ata aaa ctc agt gct gcc aca gct cag aaa gat att	1363
Asn Gly Lys Lys Ile Lys Leu Ser Ala Ala Thr Ala Gln Lys Asp Ile	
410 415 420	
cgt ata gat cgt cct gtt gta ctg gca att agc gat gag agt ttt tat	1411
Arg Ile Asp Arg Pro Val Val Leu Ala Ile Ser Asp Gly Ser Phe Tyr	
425 430 435	
caa aat ggc ttt ttg aat gag gac cat tcc tat gat ggg att ctt gag	1459
Gln Asn Gly Phe Leu Asn Glu Asp His Ser Tyr Asp Gly Ile Leu Glu	
440 445 450	
tta gat gct ggg aaa gac atc gtg att tct gca gat tct cgc agt ata	1507
Leu Asp Ala Gly Lys Asp Ile Val Ile Ser Ala Asp Ser Arg Ser Ile	
455 460 465	
gat gct gta caa tct ccg tat ggc tat cag gga aag tgg acg atc aat	1555
Asp Ala Val Gln Ser Pro Tyr Gly Tyr Gln Gly Lys Trp Thr Ile Asn	
470 475 480 485	
tgg tct act gat gat aag aaa gct acg gtt tct tgg gcg aag cag agt	1603
Trp Ser Thr Asp Asp Lys Lys Ala Thr Val Ser Trp Ala Lys Gln Ser	
490 495 500	
ttt aat ccc act gct gag cag gag gct ccg tta gtt cct aat ctt ctt	1651
Phe Asn Pro Thr Ala Glu Gln Glu Ala Pro Leu Val Pro Asn Leu Leu	
505 510 515	
tgg ggt tct ttt ata gat gtt cgt tcc ttc cag aat ttt ata gag cta	1699
Trp Gly Ser Phe Ile Asp Val Arg Ser Phe Gln Asn Phe Ile Glu Leu	
520 525 530	
ggg act gaa ggt gct cct tac gaa aag aga ttt tgg gtt gca ggc att	1747
Gly Thr Glu Gly Ala Pro Tyr Glu Lys Arg Phe Trp Val Ala Gly Ile	
535 540 545	
tcc aat gtt ttg cat agg agc ggt cgt gaa aat caa agg aaa ttc cgt	1795
Ser Asn Val Leu His Arg Ser Gly Arg Glu Asn Gln Arg Lys Phe Arg	
550 555 560 565	
cat gtg agt gga ggt gct gta gta ggt gct agc acg agg atg ccg ggt	1843
His Val Ser Gly Gly Ala Val Val Gly Ala Ser Thr Arg Met Pro Gly	
570 575 580	
ggg gat acc ttg tct ctg ggt ttt gct cag ctc ttt gcg cgt gac aaa	1891
Gly Asp Thr Leu Ser Leu Gly Phe Ala Gln Leu Phe Ala Arg Asp Lys	
585 590 595	
gac tac ttt atg aat acc aat ttc gca aag acc tac gca gga tct tta	1939
Asp Tyr Phe Met Asn Thr Asn Phe Ala Lys Thr Tyr Ala Gly Ser Leu	
600 605 610	

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Fig. 1 (con't)

cgt ttg cag cac gat gct tcc cta tac tct gtg gtg agt atc ctt tta	1987
Arg Leu Gln His Asp Ala Ser Leu Tyr Ser Val Val Ser Ile Leu Leu	
615 620 625	
gga gag gga gga ctc cgc gag atc ctg ttg cct tat gtt tcc aag act	2035
Gly Glu Gly Gly Leu Arg Glu Ile Leu Leu Pro Tyr Val Ser Lys Thr	
630 635 640 645	
ctg ccg tgc tct ttc tat ggg cag ctt agc tac ggc cat acg gat cat	2083
Leu Pro Cys Ser Phe Tyr Gly Gln Leu Ser Tyr Gly His Thr Asp His	
650 655 660	
cgc atg aag acc gag tct cta ccc ccc ccc ccc ccg acg ctc tcg acg	2131
Arg Met Lys Thr Glu Ser Leu Pro Pro Pro Pro Thr Leu Ser Thr	
665 670 675	
gat cat act tct tgg gga gga tat gtc tgg gct gga gag ctg gga act	2179
Asp His Thr Ser Trp Gly Gly Tyr Val Trp Ala Gly Glu Leu Gly Thr	
680 685 690	
cga gtt gct gtt gaa aat acc agc ggc aga gga ttt ttc caa gag tac	2227
Arg Val Ala Val Glu Asn Thr Ser Ser Gly Arg Gly Phe Phe Gln Glu Tyr	
695 700 705	
act cca ttt gta aaa gtc caa gct gtt tac gct cgc caa gat agc ttt	2275
Thr Pro Phe Val Lys Val Gln Ala Val Tyr Ala Arg Gln Asp Ser Phe	
710 715 720 725	
gta gaa cta gga gct atc agt cgt gat ttt agt gat tcg cat ctt tat	2323
Val Glu Leu Gly Ala Ile Ser Arg Asp Phe Ser Asp Ser His Leu Tyr	
730 735 740	
aac ctt gcg att cct ctt gga atc aag tta gag aaa cgg ttt gca gag	2371
Asn Leu Ala Ile Pro Leu Gly Ile Lys Leu Glu Lys Arg Phe Ala Glu	
745 750 755	
caa tat tat cat gtt gta gcg atg tat tct cca gat gtt tgt cgt agt	2419
Gln Tyr Tyr His Val Val Ala Met Tyr Ser Pro Asp Val Cys Arg Ser	
760 765 770	
aac ccc aaa tgt acg act acc cta ctt tcc aac caa ggg agt tgg aag	2467
Asn Pro Lys Cys Thr Thr Leu Leu Ser Asn Gln Gly Ser Trp Lys	
775 780 785	
acc aaa ggt tcg aac tta gca aga cag gct ggt att gtt cag gcc tca	2515
Thr Lys Gly Ser Asn Leu Ala Arg Gln Ala Gly Ile Val Gln Ala Ser	
790 795 800 805	
ggg ttt cga tct ttg gga gct gca gca gag ctt ttc ggg aac ttt ggc	2563
Gly Phe Arg Ser Leu Gly Ala Ala Ala Glu Leu Phe Gly Asn Phe Gly	
810 815 820	

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Fig. 1 (con't)

ttt gaa tgg cgg gga tct tct cgt agc tat aat gta gat gcg ggt agc	2611
Phe Glu Trp Arg Gly Ser Ser Arg Ser Tyr Asn Val Asp Ala Gly Ser	
825 830 835	
aaa atc aaa ttt tagcgatttc tctttcgatg ctattttttcc atggctattt	2663
Lys Ile Lys Phe	
840	
ttaaaaatgat agccatgggt atagatacgt agtccttatt tcaaagaaga cactgttgca	2723
ttagatacgc tctctgatcc ctcaaaa	2750

Figure 2 (RY-32)

Restriction Enzyme analysis of CPN100397

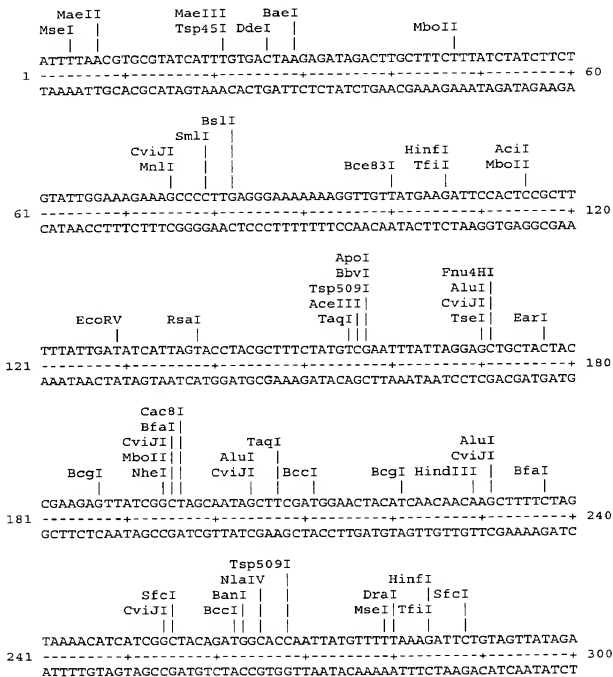


Fig. 2 (cont')

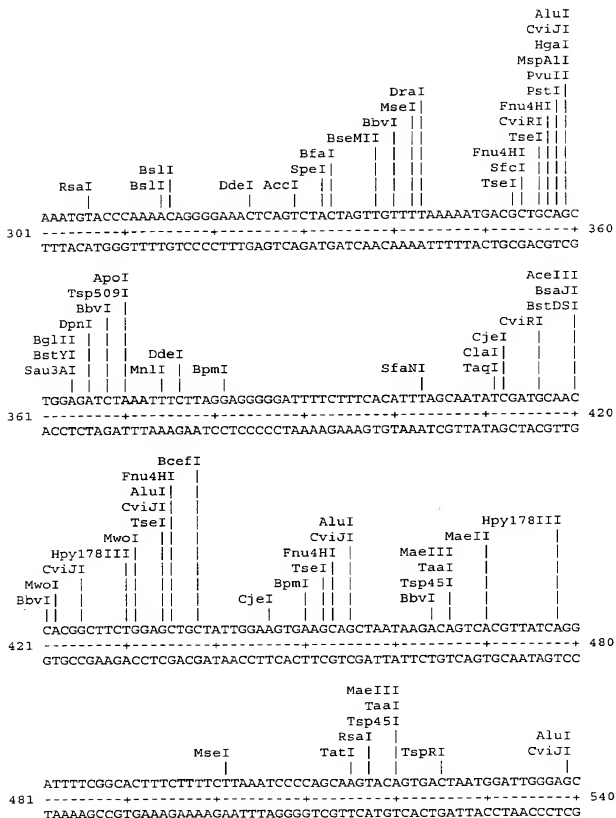


Fig. 2 (con't)

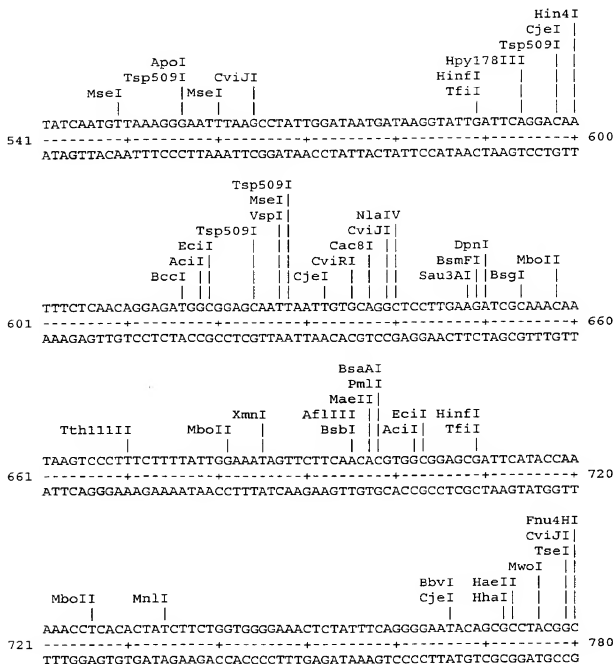
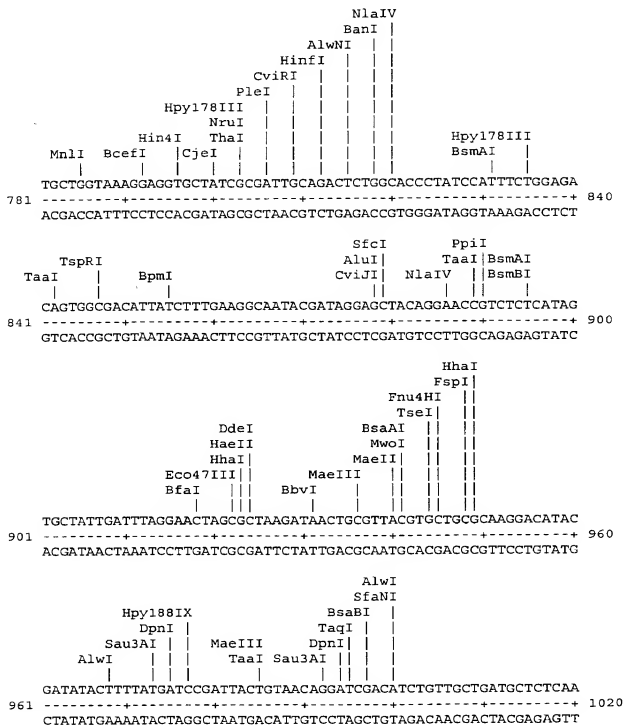


Fig. 2 (cont')





DrdII  
NlaIV  
BscGI  
BpmI  
MseI  
VspI  
SspI  
CviJI  
BslI  
BsrI  
Sth132I  
AccI  
Hpy178III  
TATTAATAGCCCTGATACTGGAGATAACAAAGAGTATACGGGAACCATAGTCTTTTCTGG  
1021  
ATAATTATCGGGACTATGACCTCTATTGTTTCTCATATGCCCTTGGTATCAGAAAAGACC  
AluI  
CviJI  
MnlI  
Hin4I  
AluI  
BpII  
CviJI  
BpmI  
AciI  
MboII  
Tsp509I  
AGAGAAGCTCACGGAGGCGAAGCTTAAAGATGAGAAGAACCGCACTTCTAAATTACTTCA  
1081  
TCTCTTCGAGTGCCTCCGTCTTCGATTCTACTCTTCTTGGCGTGAAGATTTAATGAAGT  
DraI  
MseI  
TaaI  
SfcI  
BsmFI  
MseI  
HphI  
MseI  
AAATGTTGCTTTTAAAAATGGGACTGTGATGTTTTAAAGGTGATGCTGCTTTTAAAGTGC  
1141  
TTTACAACGAAATTTTACCTTGACATCAAAATTTCCACTACAGCAAAATTCACGCTT  
Hpy178III  
FokI  
SfaNI  
PpiI  
TaaI  
XmnI  
DdeI  
Hin4I  
CviRI  
DdeI  
BseMII  
DdeI  
AatII  
BsaHI  
MaeII  
CviRI  
BsmFI  
CGGTTTCTCTCAGGATGCAAACTCTAAGTTGATTATGGATTAGGGACGTCGTGTTGTC  
1201  
GCCAAAGAGAGTCTACGTTTGAGATTCAACTAATACCTAAATCCCTGCAGCAACCAACG  
ApoI  
Tsp509I  
HincII  
Tth111II  
HpaI  
TaqI  
MseI  
PleI  
MseI  
VspI  
Tsp509I  
HinfI  
Hpy178III  
DdeI  
Sth132I  
BscGI  
AAACACCGAAAGTATCGAGTTAAGCAATTTGGAAATTAATATAGACTCTCTCAGGAACGG  
1261  
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Fig. 2 (con't)

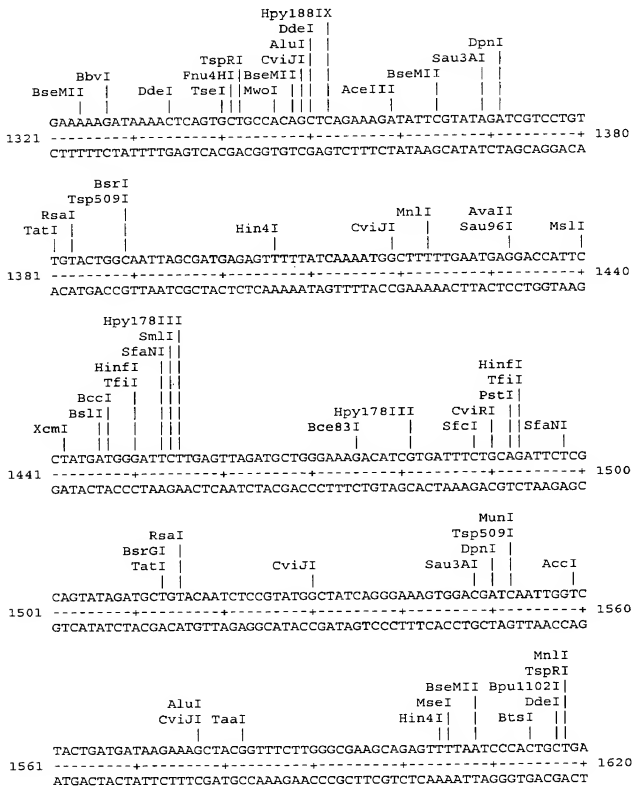


Fig. 2 (con't)

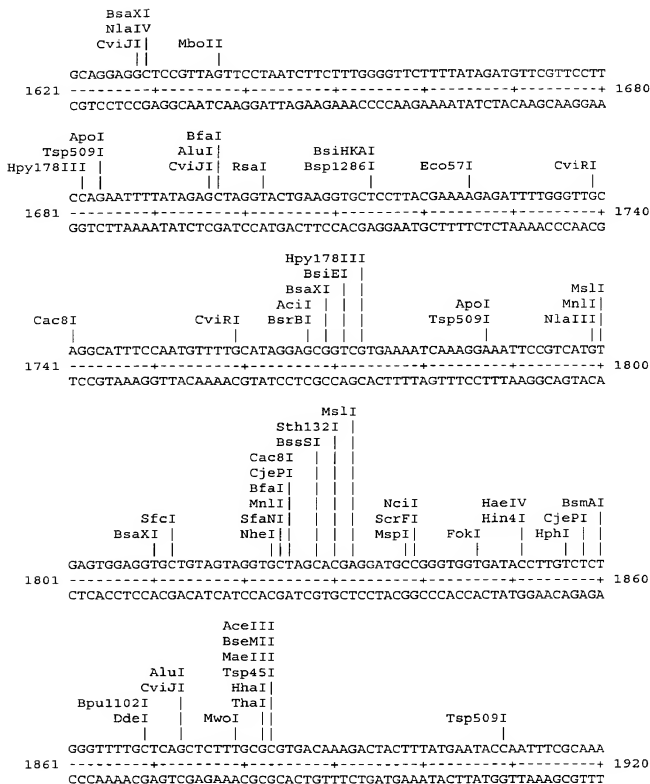


Fig. 2 (con't)

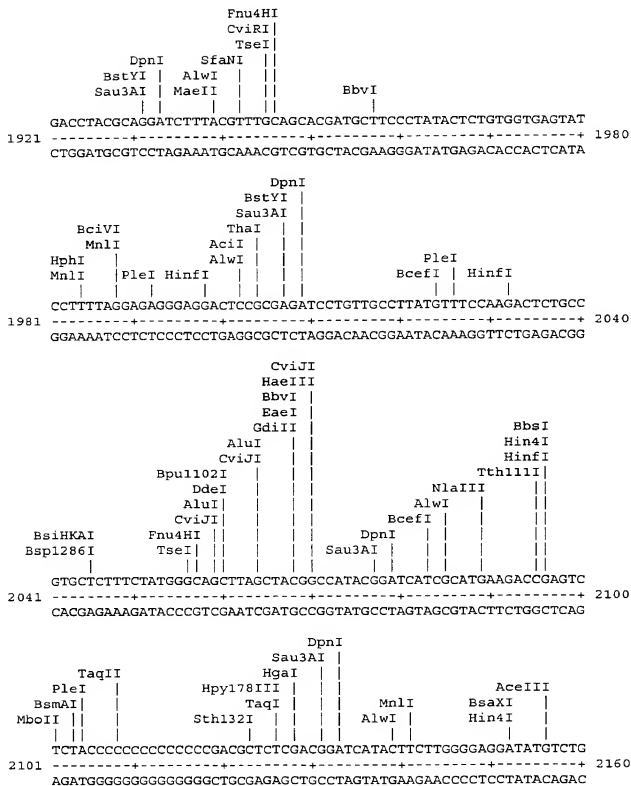


Fig. 2 (cont')

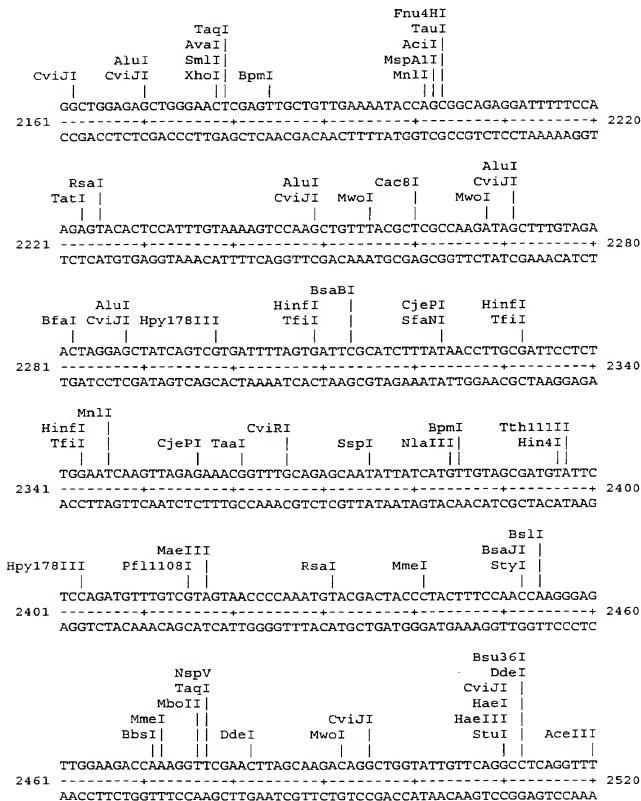


Fig. 2 (cont')

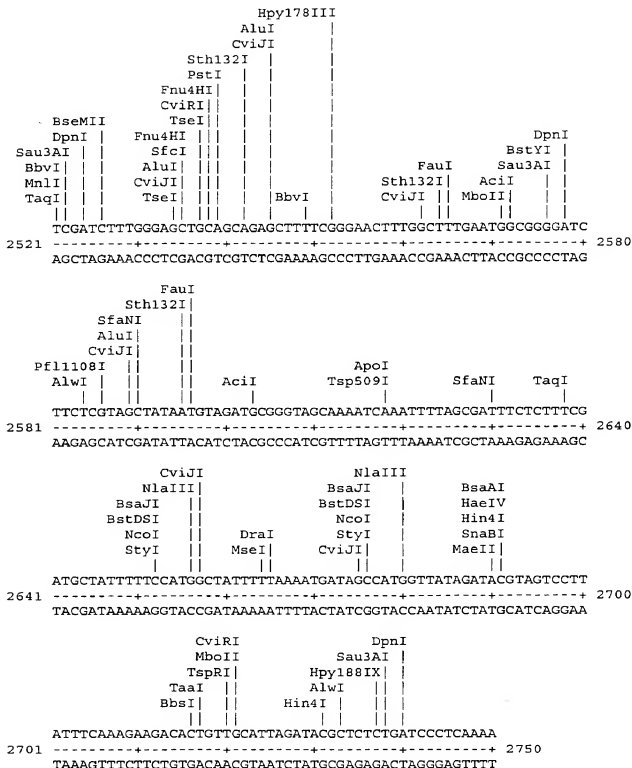


Figure 3: CPN100421

```

ctctgtccc tcgctgtgc aacctacccc tcttccctcg aattetaate ctttgaacgt 60
agtaacaacag cctgttgctg catcgtcagt gccttccctac atg ccc cca ctg aat 115
Met Pro Pro Leu Asn
1 5

gct gat gat gtt ctc cct aga gac cat ctg tca gat gga agt ttc tca 163
Ala Asp Asp Val Leu Pro Arg Asp His Leu Ser Asp Gly Ser Phe Ser
10 15 20

gat acg tat cca gac att aca acg caa gcg atc atc tta att ttc ttg 211
Asp Thr Tyr Pro Asp Ile Thr Thr Gln Ala Ile Ile Leu Ile Phe Leu
25 30 35

gcc cta tcg cct ttc ctg gtc atg ttg ctc act tcg tat cta aag att 259
Ala Leu Ser Pro Phe Leu Val Met Leu Leu Thr Ser Tyr Leu Lys Ile
40 45 50

atc att act tta gtc tta tta cgt aac gcc tta gga gta caa caa aca 307
Ile Ile Thr Leu Val Leu Leu Arg Asn Ala Leu Gly Val Gln Gln Thr
55 60 65

cct ccc agt caa gtc ctc aat ggg att gca ctc atc cta tct att tat 355
Pro Pro Ser Gln Val Leu Asn Gly Ile Ala Leu Ile Leu Ser Ile Tyr
70 75 80 85

gtg atg ttc ccc acg gga gtg gct atg tat aaa gat gct cgc aag gaa 403
Val Met Phe Pro Thr Gly Val Ala Met Tyr Lys Asp Ala Arg Lys Glu
90 95 100

atc gaa gcc aat acc att cct caa agc ctc ttc act gca gaa ggt gct 451
Ile Glu Ala Asn Thr Ile Pro Gln Ser Leu Phe Thr Ala Glu Gly Ala
105 110 115

gaa aca gtg ttt gtc gct tta aac aaa tct aaa gaa cct ttg cgc tct 499
Glu Thr Val Phe Val Ala Leu Asn Lys Ser Lys Glu Pro Leu Arg Ser
120 125 130

ttc tta att cgc aac act cca aaa gca caa att caa agc ttt tac aag 547
Phe Leu Ile Arg Asn Thr Pro Lys Ala Gln Ile Gln Ser Phe Tyr Lys
135 140 145

atc tca cag aaa acc ttc cct tcg gaa att cga gcg cac ctc act gcc 595
Ile Ser Gln Lys Thr Phe Pro Ser Glu Ile Arg Ala His Leu Thr Ala
150 155 160 165

tcc gac ttt gta atc att att cct gct ttt att atg ggt cag ata aaa 643
Ser Asp Phe Val Ile Ile Ile Pro Ala Phe Ile Met Gly Gln Ile Lys
170 175 180

aat gct ttc gaa att gga gtc ttg atc tat cta cct ttc ttt gtt att 691
Asn Ala Phe Glu Ile Gly Val Leu Ile Tyr Leu Pro Phe Phe Val Ile
185 190 195

```

Title: CHLAMYDIA ANTIGENS AND  
CORRESPONDING DNA FRAGMENTS  
AND USES THEREOF

Inventor(s): Andrew D. MURDIN et al  
DOCKET NO.: 032931/0251

WO 00/24765

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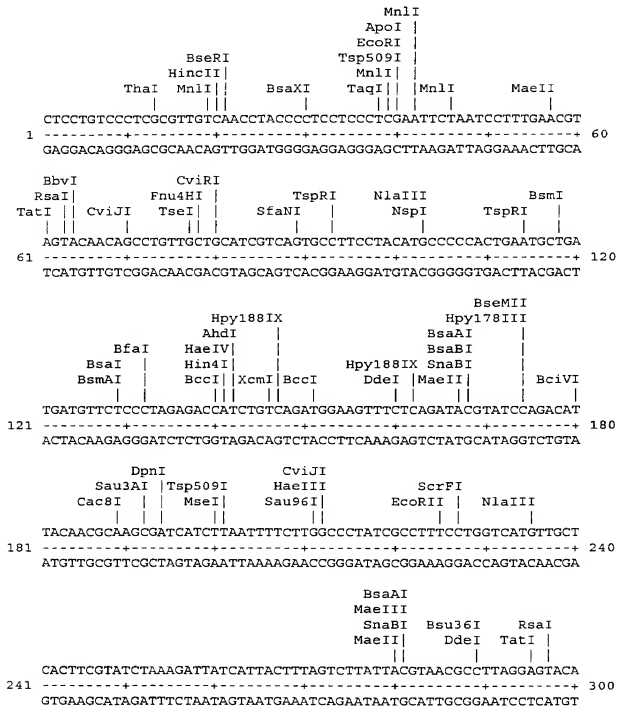
Fig. 3 (con't)

gat tta gtg act gct aac gtt ctt gta gcg atg cag atg atg atg tta	739
Asp Leu Val Thr Ala Asn Val Leu Val Ala Met Gln Met Met Met Leu	
200 205 210	
tcc cct cta tcg att tcg tta cct tta aag tta ctt ttg atc gtc atg	787
Ser Pro Leu Ser Ile Ser Leu Pro Leu Lys Leu Leu Leu Ile Val Met	
215 220 225	
gta gac gga tgg aca tta ctg ctc caa ggg ctt atg atc agc ttt aaa	835
Val Asp Gly Trp Thr Leu Leu Leu Gln Gly Leu Met Ile Ser Phe Lys	
230 235 240 245	
taaggacacg tgccgtgtta gcatttttcg caactagttt caaatctgtt ctttttgagt	895
actcctacca atcattatta cttattttga ttgtttcggc acctcccatc atcttagctt	955
ccatagtcgg gattatgggt gcgatcttcc aagccgcaac acaaa	1000



Figure 4 (RY-34)

Restriction enzyme analysis of CP100421



MnlI  
 Tth111III  
 BmrI  
 BsrI  
 FokI  
 MnlI  
 CviRI  
 Sth132I

301  
 ACAAACACCTCCAGTCAGTCAAGTCTCAATGGGATTGCACCTCATCTATCTATTATGTGAT  
 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+  
 TGTTTTGTGGAGGGTCAGTTTCAGGAGTTACCCCTAACGTGAGTAGGATAGATAAAATACACTA  
 360

SfaNI  
 CviJI  
 BstXI  
 MslI  
 BscGI  
 BsaJI  
 BstDSI  
 BcgI  
 Cae8I  
 TaqI  
 CjePI  
 CviJI  
 BcgI

361  
 GTTCCCCACGGGAGTGGCTATGTATAAAGATGCTCGCAAGGAAATCGAAGCCAATACCAT  
 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+  
 CAAGGGGTGCGCTCACCAGATACATATTTCTACGAGCGTTCCTTTAGCTTCGGTTATGGTA  
 420

Tth111III  
 BstAPI  
 PstI  
 TspRI  
 CviRI  
 MnlI  
 BtsI  
 SfcI  
 EarI  
 CjePI  
 MboII  
 CviJI  
 MwoI  
 TspRI  
 DraI  
 MseI

421  
 TCCTCAAAGCCTCTTCACTGCAGAAAGTGCTGAAACAGTGTTTGTGCGCTTTAAACAAATC  
 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+  
 AGGAGTTTCGGAGAAGTGACGTCTTCCAGACTTTGTCAAAACAGCGAAATTTGTTTAG  
 480

AluI  
 CviJI  
 HhaI  
 Tsp509I  
 MseI  
 BsbI  
 ApoI  
 Tsp509I  
 HindIII

481  
 TAAAGAACCTTTGCGCTCTTTCTTAATTTCGCAACACTCCAAAAGCACAAATTCAAAGCTT  
 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+  
 ATTTCTTGGAAACGCGAGAAAGAATTAAAGCGTTGTGAGGTTTTCGTGTTTAAGTTTCGAA  
 540



Fig. 4 (con't)

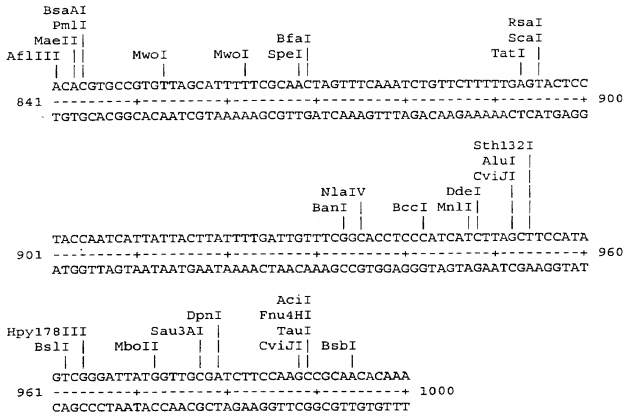


Figure 5:

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tagctttata caaagtatat aaaaataaca cgacaataaa aggagcgggtg ttttctcttc 60

tgaggtaaat cagcctcaaa gatactacgc catagtaaag atg aag ttt ttt agc 115
Met Lys Phe Phe Ser
1 5

tta att ttt aaa gat gat gat gtc tcc cca aat aag aag gtt tta tct 163
Leu Ile Phe Lys Asp Asp Val Ser Pro Asn Lys Lys Val Leu Ser
10 15 20

cct gaa gct ttc tct gct ttc ctt gat gcc aaa gag ctg tta gaa aaa 211
Pro Glu Ala Phe Ser Ala Phe Leu Asp Ala Lys Glu Leu Leu Glu Lys
25 30 35

aca aaa gcc gat agc gaa gcc tat gtt gca gag aca gaa caa aag tgt 259
Thr Lys Ala Asp Ser Glu Ala Tyr Val Ala Glu Thr Glu Gln Lys Cys
40 45 50

gca caa att cgt caa gaa gct aaa gat caa gga ttt aaa gag gga tct 307
Ala Gln Ile Arg Gln Glu Ala Lys Asp Gln Gly Phe Lys Glu Gly Ser
55 60 65

gaa tcc tgg agc aag caa att gct ttc tta gaa gaa gaa act aaa aat 355
Glu Ser Trp Ser Lys Gln Ile Ala Phe Leu Glu Glu Thr Lys Asn
70 75 80 85

cta cgc ata aga gta cgc gag gcc ttg gtt cct ctg gca att gcg agt 403
Leu Arg Ile Arg Val Arg Glu Ala Leu Val Pro Leu Ala Ile Ala Ser
90 95 100

gtg agg aaa atc att ggg aag gaa ctc gaa tta cat cct gaa act att 451
Val Arg Lys Ile Ile Gly Lys Glu Leu Glu Leu His Pro Glu Thr Ile
105 110 115

gtc tct att att tct caa gca ttg aaa gag ctc aca caa aat aaa cat 499
Val Ser Ile Ile Ser Gln Ala Leu Lys Glu Leu Thr Gln Asn Lys His
120 125 130

atc att atc tct gtc aat ccc aaa gat tta cct ctt gtt gag aaa agt 547
Ile Ile Ile Ser Val Asn Pro Lys Asp Leu Pro Leu Val Glu Lys Ser
135 140 145

cgt cct gaa ctc aag aac atc gtg gag tat gct gac tcc tta att ctt 595
Arg Pro Glu Leu Lys Asn Ile Val Glu Tyr Ala Asp Ser Leu Ile Leu
150 155 160 165

aca gca aaa cct gat gtt act cct ggg ggt tgc att atc gag act gaa 643
Thr Ala Lys Pro Asp Val Thr Pro Gly Gly Cys Ile Ile Glu Thr Glu
170 175 180

gca ggg atc atc aat gcg cag ctt gat gta caa tta gat gcc tta gaa 691
Ala Gly Ile Ile Asn Ala Gln Leu Asp Val Gln Leu Asp Ala Leu Glu
185 190 195

```

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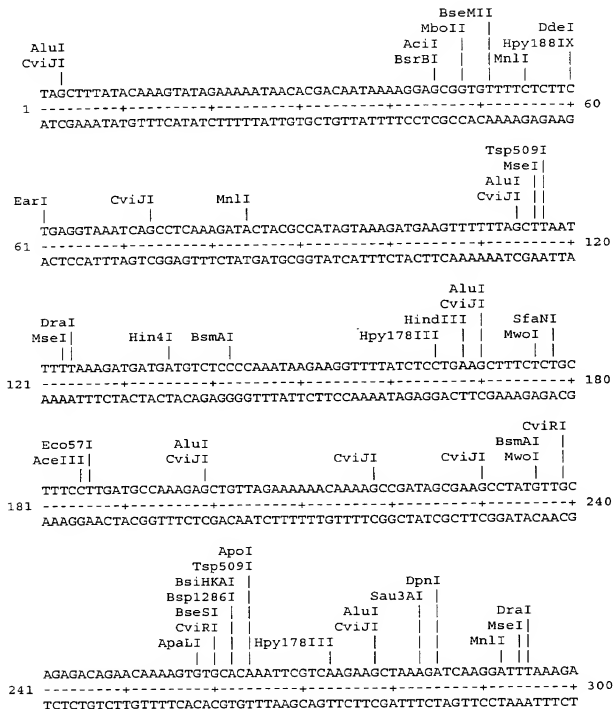
PCT/CA99/00992

Fig. 5 (con't)

aaa gct ttc tcg act ata cta aaa gcg aag aac cct gta gac gag cca	739
Lys Ala Phe Ser Thr Ile Leu Lys Ala Lys Asn Pro Val Asp Glu Pro	
200 205 210	
tct gag act tca tca tcc acg gat tct tct tct tta tct aat gat cag	787
Ser Glu Thr Ser Ser Ser Thr Asp Ser Ser Ser Leu Ser Asn Asp Gln	
215 220 225	
gat aag aaa gaa taaaggattt cactattatg cgatecattt ttcgattttc	839
Asp Lys Lys Glu	
230	
cctttgtttt tttaacgctga gcgtctcatg ctgatttgct gacgccagtc tatatgaaaa	899
c	900

Figure 6 (RY-35)

Restriction analysis of CPN100422



Inventor(s): Andrew D. MURDIN et al  
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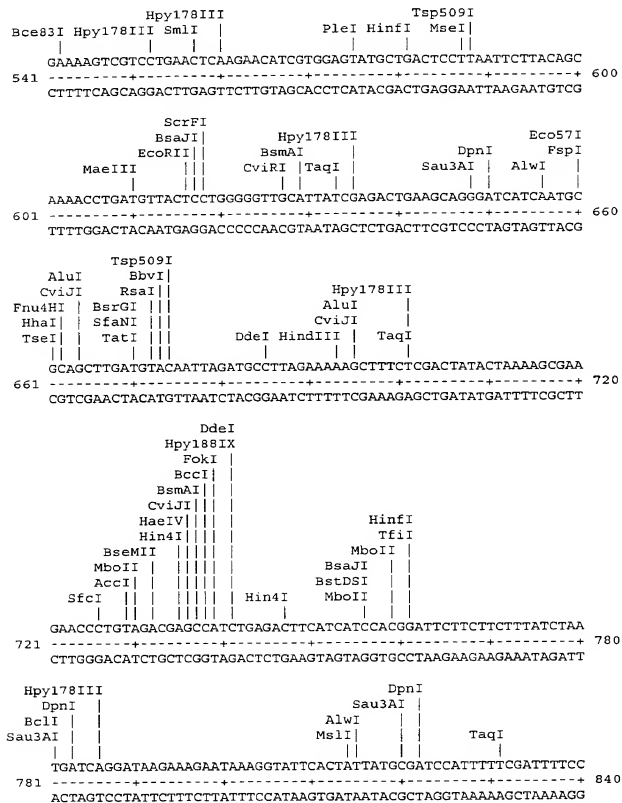
PCT/CA99/00992

Fig. 6 (con't)

SrfI  
 EcoRI  
 AlwI  
 HinfI  
 TfiI  
 BsaBI  
 Hpy188IX  
 DpnI  
 BstYI  
 Sau3AI  
 Tsp509I  
 Cac8I  
 Tth111II  
 BpmI  
 DdeI  
 MboII  
 MboII  
 GGGATCTGAATCCTGGAGCAAGCAAATGGCTTCTTAGAAGAAGAACTAAAAATCTACG  
 301 +-----+-----+-----+-----+-----+-----+-----+-----+-----+  
 CCCTAGACTTAGGACCTCGTTCGTTTAACGAAAGAATCTTCTTCTTGATTTTATAGTGC 360  
 BsaJI  
 StyI  
 CviJI  
 HaeI  
 HaeIII  
 CjePI  
 MnlI  
 RsaI  
 MnlI  
 StuI  
 NlaIV  
 DrdII  
 MnlI  
 MnlI  
 Tsp509I  
 CATAAGAGTAGCGGAGGCCTTGGTTCCTCTGGCAATTGCGAGTGTGAGGAAAATCATTGG  
 361 +-----+-----+-----+-----+-----+-----+-----+-----+-----+  
 GTATTCTCATGCGCTCGGAACCAAGGAGACCGTTAACGCTCACACTCCTTTTAGTAACC 420  
 Hpy178III  
 CjePI  
 Tsp509I  
 FokI  
 TaqI  
 Bce83I  
 BsmAI  
 SmlI  
 GAAGGAACTCGAATTACATCTCGAAACTATTGTCTCTATTATTCTCAAGCATTGAAAGA  
 421 +-----+-----+-----+-----+-----+-----+-----+-----+-----+  
 CTTCCTTGAGCTTAATGTAGGACTTTGATAACAGAGATAATAAAGAGTTCGTAACCTTCT 480  
 BanII  
 BsiHKAI  
 Bsp1286I  
 SacI  
 Tth111II  
 AluI  
 CviJI  
 MnlI  
 GCTCACACAAAATAACATATCATTTATCTCTGTCAATCCCAAAGATTACCTCTTGTTGA  
 481 +-----+-----+-----+-----+-----+-----+-----+-----+-----+  
 CGAGTGTGTTTATTGTATAGTAATAGAGACAGTTAGGTTTCTAAATGGAGAACAACT 540



Fig. 6 (cont)



[illegible]

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Figure 7: CPN 100424

tgctcgcat	tggcactaat	ccccctttt	ggtatggtga	ataaaaagg	atgcgtggat	60
tatgggtcgt	cgatctattt	cttttgcctt	gttctttcta	atg aca ttg ctg tgc		115
				Met Thr Leu Leu Cys		
				1	5	
tgt aca agc tgt	aac agc agg tct	cta att gtg cac	ggt ctt cct ggc			163
Cys Thr Ser Cys	Asn Ser Arg Ser	Leu Ile Val His	Gly Leu Pro Gly			
	10	15	20			
aga gaa gcg aat	gag att gtg gtg	ctt ttg gta agc	aaa ggg gtg gct			211
Arg Glu Ala Asn	Glu Ile Val Val	Leu Leu Val Ser	Lys Gly Val Ala			
	25	30	35			
gca caa aaa ttg	cct caa gct gca	gcg gct aca gcc	gga gca gct act			259
Ala Gln Lys Leu	Pro Gln Ala Ala	Ala Ala Thr Ala	Gly Ala Ala Thr			
	40	45	50			
gag caa atg tgg	gat atc gcg gtt	ccg tca gca caa	atc aca gag gcc			307
Glu Gln Met Trp	Asp Ile Ala Val	Pro Ser Ala Gln	Ile Thr Glu Ala			
	55	60	65			
ctt gcc att cta	aat caa gcg ggt	ctt cca cgt atg	aaa ggg aca agc			355
Leu Ala Ile Leu	Asn Gln Ala Gly	Leu Pro Arg Met	Lys Gly Thr Ser			
	70	75	80			85
ctg tta gat ctt	ttt gca aaa caa	ggt ctt gtt cct	tcc gag ctt cag			403
Leu Leu Asp Leu	Phe Ala Lys Gln	Gly Leu Val Pro	Ser Glu Leu Gln			
	90	95	100			
gaa aaa atc cgt	tat caa gaa ggc	tta tca gaa cag	atg gcc tct acg			451
Glu Lys Ile Arg	Tyr Gln Glu Gly	Leu Ser Glu Gln	Met Ala Ser Thr			
	105	110	115			
att aga aaa atg	gat ggc gtt gtc	gat gcc tca gta	cag att tcc ttc			499
Ile Arg Lys Met	Asp Gly Val Val	Asp Ala Ser Val	Gln Ile Ser Phe			
	120	125	130			
act aca gaa aat	gaa gat aat ctt	cct tta aca gcc	tct gtg tat att			547
Thr Thr Glu Asn	Glu Asp Asn Leu	Pro Leu Thr Ala	Ser Val Tyr Ile			
	135	140	145			
aag cat cga ggg	gtt ttg gac aat	ccg aac agc att	atg gtt tcc aaa			595
Lys His Arg Gly	Val Leu Asp Asn	Pro Asn Ser Ile	Met Val Ser Lys			
	150	155	160			165
att aag cgc ctt	att gca agt gct	gtt cca gga ctt	gtg cca gag aac			643
Ile Lys Arg Leu	Ile Ala Ser Ala	Val Pro Gly Leu	Val Pro Glu Asn			
	170	175	180			
gtc tct gta gtg	agc gat cgc gca	gct tat agt gat	att aca att aat			691
Val Ser Val Val	Ser Asp Arg Ala	Ala Tyr Ser Asp	Ile Thr Ile Asn			
	185	190	195			

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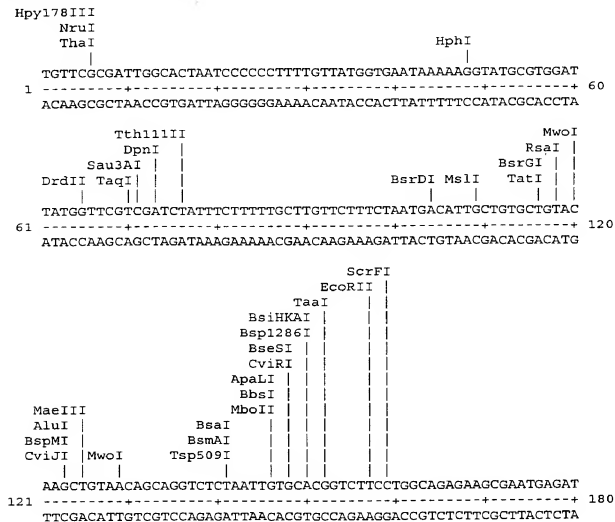
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Fig. 7 (con't)

ggt cct tgg gga tta aca gaa gaa atc gat tat gtt tct gtt tgg ggt	739
Gly Pro Trp Gly Leu Thr Glu Glu Ile Asp Tyr Val Ser Val Trp Gly	
200 205 210	
att att ctt gcg aag tct tgc etc acc aaa ttc cgt etc att ttt tat	787
Ile Ile Leu Ala Lys Ser Ser Leu Thr Lys Phe Arg Leu Ile Phe Tyr	
215 220 225	
gtc ttg att etc att tta ttt gtt att tct tgt ggt etc ctt tgg gtc	835
Val Leu Ile Leu Ile Leu Phe Val Ile Ser Cys Gly Leu Leu Trp Val	
230 235 240 245	
att tgg aaa act cat act etc att atg act atg gga ggt aca aaa ggg	883
Ile Trp Lys Thr His Thr Leu Ile Met Thr Met Gly Gly Thr Lys Gly	
250 255 260	
ttc ttc aac cct aca cca tat aca aag aat gcc ttg gaa gcc aag aaa	931
Phe Phe Asn Pro Thr Pro Tyr Thr Lys Asn Ala Leu Glu Ala Lys Lys	
265 270 275	
gcc gag gga gca gct gct gac aaa gag aaa aaa gaa gat gca gat tca	979
Ala Glu Gly Ala Ala Ala Asp Lys Glu Lys Lys Glu Asp Ala Asp Ser	
280 285 290	
cag ggg gaa agc aaa aat gcg gaa acc agt gat aaa gac tct agt gat	1027
Gln Gly Glu Ser Lys Asn Ala Glu Thr Ser Asp Lys Asp Ser Ser Asp	
295 300 305	
aaa gat gct cca gaa gga agc aat gaa att gag ggt gct tagtgactgc	1076
Lys Asp Ala Pro Glu Gly Ser Asn Glu Ile Glu Gly Ala	
310 315 320	
caacactttt ggaactctag acatcttgat gaagcactcc aaggaagatg acctctccag	1136
gtttcttctt aaaaatcttc ttgttgaatc tectcatccc gaagaaaatc ctttaaaatc	1196
ttta	1200

Figure 8 (RY-36)

Restriction analysis of CPN100424



SfiI  
 CviJI  
 Fnu4HI  
 TauI  
 AclI  
 MspAII  
 MwoI  
 PstI  
 Fnu4HI  
 MnlI  
 CviRI  
 TseI  
 Tsp509I  
 CviRI  
 Bce83I  
 Fnu4HI  
 BbvI  
 BsgI  
 CviJI  
 TseI  
 BbvI  
 SmlI  
 TseI  
 Fnu4HI  
 SfcI  
 AluI  
 CviJI  
 TseI  
 DdeI  
 AlwNI  
 RleAI  
 AluI  
 CviJI  
 Fnu4HI  
 CjePI  
 MwoI  
 TseI  
 BseMII  
 MspI  
 BbvI  
 CviJI  
 MwoI  
 BbvI  
 EcoRV  
 NlaIV  
 CjePI  
 AcII  
 Thai  
 MnlI  
 TACAGCCGGAGCAGCTACTGAGCAAAATGTGGGATATCGCGGTTCGCTCAGCACAAATCAC  
 ATGTCGGCCTCGTCGATGACTCGTTTACACCCCTATAGCGCCAAAGGCAGTCGTGTTAGTG  
 CviJI  
 HaeIII  
 CjePI  
 EcoO109I  
 Sau96I  
 SthI32I  
 FauI  
 SimI  
 AcII  
 BbsI  
 MboII  
 BsaAI  
 CjePI  
 MaeII  
 CviJI  
 AGAGGCCCTTGCCATTCTAAATCAAGCGGTCTTCCAGGTATGAAAGGGACAAGCCTGTT  
 TCTCCGGGAACGGTAAGATTTAGTTCGCCCCAGAAGGTGCATACTTCCCTGTTTCGGACAA

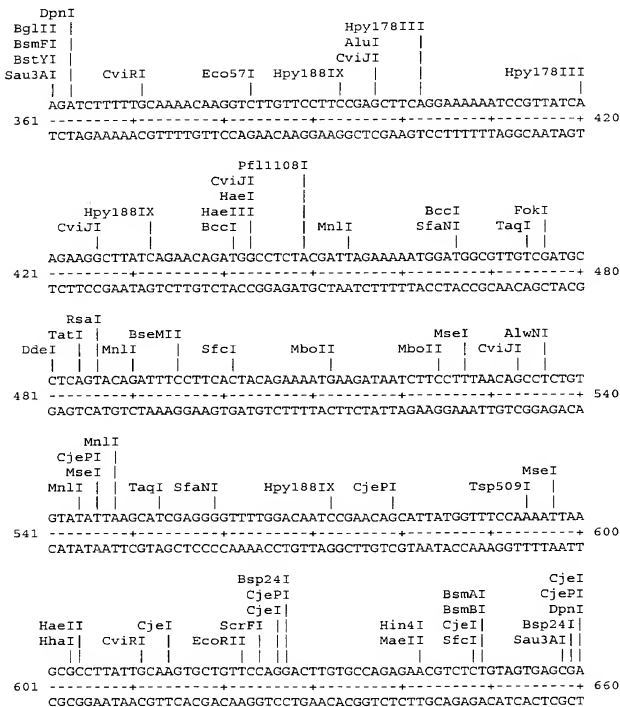


Fig. 8 (con't)

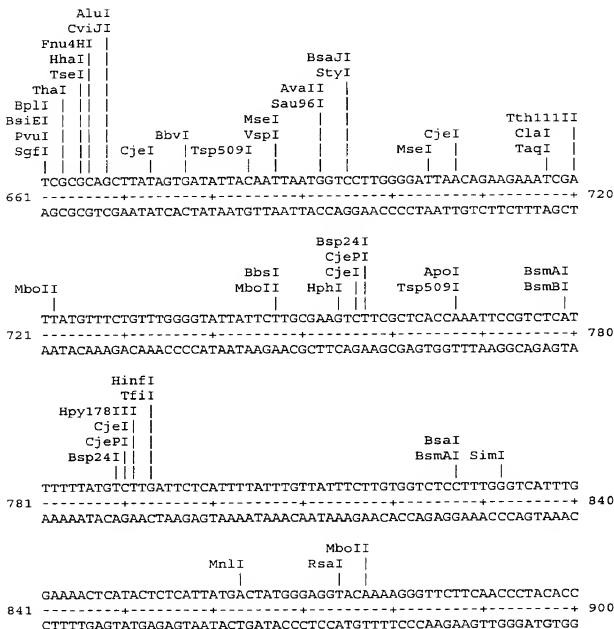
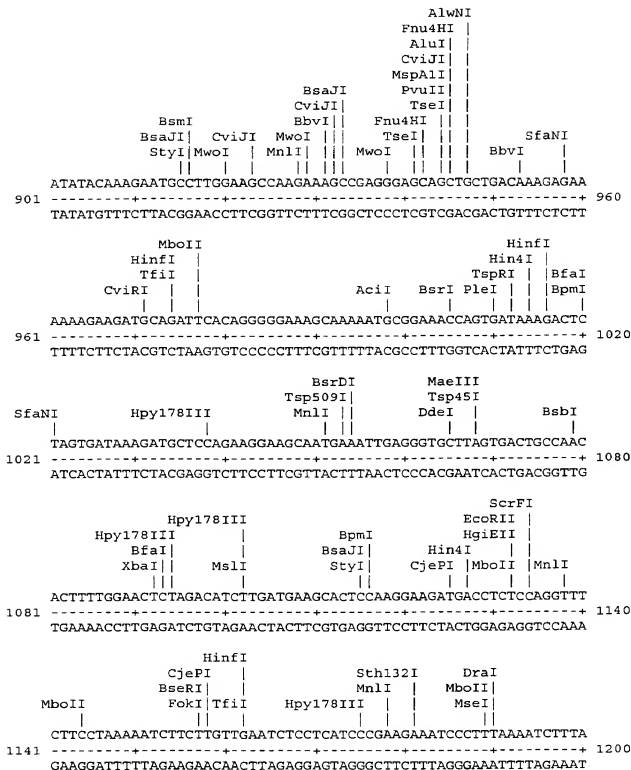




Fig. 8 (cont')



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Figure 9: CPN100426

```

tggaacccta tggaaatgta tcttatttgt gctgggctat atttcttaac gacaacatca 60
ttttctctgta ttctctagggtt atcagaaaag agaaggagtt atg aca att aga gtc 115
Met Thr Ile Arg Val
1 5

cga aac ctt gcc tac tct gta aat aag aaa aag att cta gat ggt gta 163
Arg Asn Leu Ala Tyr Ser Val Asn Lys Lys Lys Ile Leu Asp Gly Val
10 15 20

act ttt tct tta gag cga ggg cac att aca ctg ttt gtt ggg aag agt 211
Thr Phe Ser Leu Glu Arg Gly His Ile Thr Leu Phe Val Gly Lys Ser
25 30 35

ggg tca gga aaa aca atg att tta cgt gct ttg gcg ggc tta gtc cag 259
Gly Ser Gly Lys Thr Met Ile Leu Arg Ala Leu Ala Gly Leu Val Gln
40 45 50

ccc act caa gga gat att tgg att gaa ggg gag gct cca gct cta gtt 307
Pro Thr Gln Gly Asp Ile Trp Ile Glu Gly Glu Ala Pro Ala Leu Val
55 60 65

ttc caa caa ccc gag tta ttt tcc cat atg aca gta tta gga aat tgc 355
Phe Gln Gln Pro Glu Leu Phe Ser His Met Thr Val Leu Gly Asn Cys
70 75 80 85

acc cat cca caa atc cat atc aag ggt cgt agt acc gaa gaa gct cga 403
Thr His Pro Gln Ile His Ile Lys Gly Arg Ser Thr Glu Glu Ala Arg
90 95 100

gaa aag gcg ttc gag ctt tta cat ttg ttg gat att gaa gag gtt gct 451
Glu Lys Ala Phe Glu Leu Leu His Leu Leu Asp Ile Glu Glu Val Ala
105 110 115

aag aat tat cct gac cag ctg tct ggg gga caa aaa caa cgt gtg gct 499
Lys Asn Tyr Pro Asp Gln Leu Ser Gly Gly Gln Lys Gln Arg Val Ala
120 125 130

att gta cgt tct tta tgt atg gat aaa cat aca tta ctt ttt gat gaa 547
Ile Val Arg Ser Leu Cys Met Asp Lys His Thr Leu Leu Phe Asp Glu
135 140 145

cct aca tcg gct tta gat cct ttt gct acg gca tcg ttc cga cat ctt 595
Pro Thr Ser Ala Leu Asp Pro Phe Ala Thr Ala Ser Phe Arg His Leu
150 155 160 165

tta gaa aca ctt cga gac cag gaa ctg act gta ggg tta act act cat 643
Leu Glu Thr Leu Arg Asp Gln Glu Leu Thr Val Gly Leu Thr Thr His
170 175 180

gac atg caa ttt gtt cat agt tgt ttg gat cgt atc tat ctt ata gat 691
Asp Met Gln Phe Val His Ser Cys Leu Asp Arg Ile Tyr Ile Asp
185 190 195

```

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Fig. 9 (con't)

```
caa gga act gtt gcg ggg gtc tat gac aag cgt gac gga gag ctc gat 739
Gln Gly Thr Val Ala Gly Val Tyr Asp Lys Arg Asp Gly Glu Leu Asp
      200                      205                      210

tct ggt cat cca tta tcg aaa tat atc cac tct gct caa taggactaca 788
Ser Gly His Pro Leu Ser Lys Tyr Ile His Ser Ala Gln
      215                      220                      225

gctgctagag cagctgtagt gatacttttag aatcctgacc agtggcagga atgagcggca 848

tg                                                                    850
```

Figure 10 (RY-37)  
Restriction enzyme analysis of CPN100426

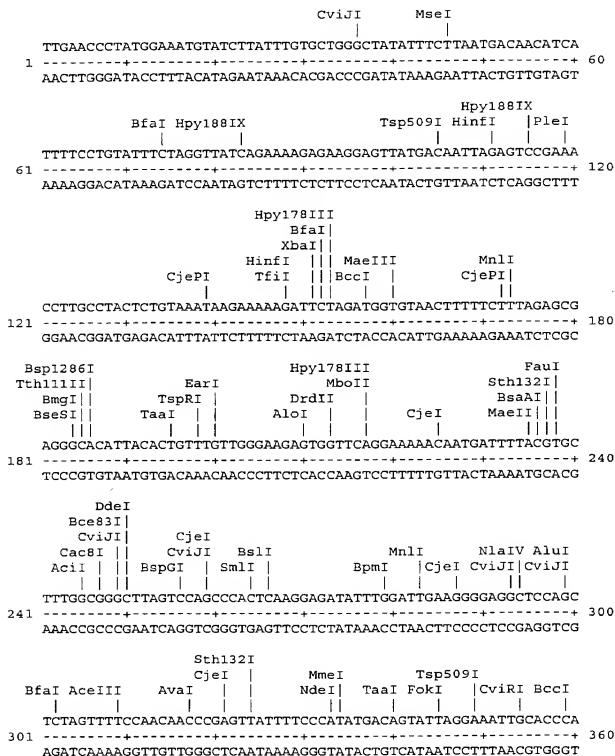


Fig. 10 (con't)



Fig. 10 (cont)

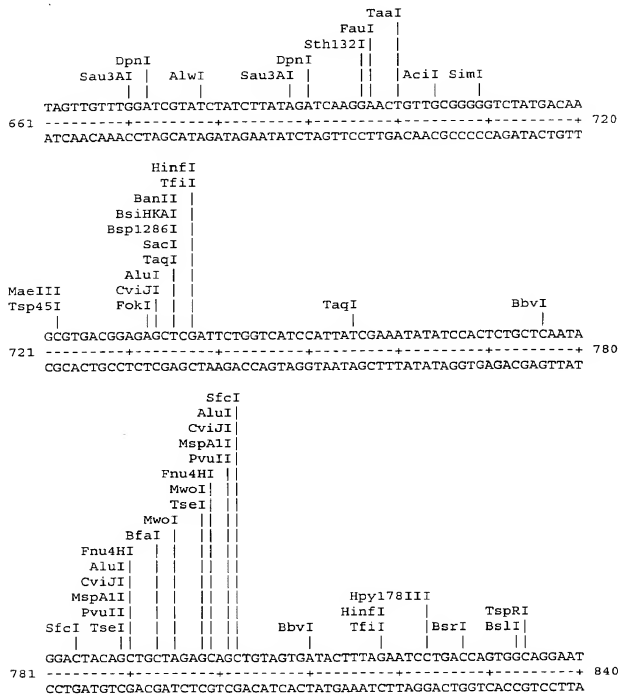


Fig. 10 (con't)

```
Fnu4HI
TauI
AclI |
BsrBI | NlaIII
      | | |
      GAGCGGCATG
841 -----+ 850
      CTCGCCGTAC
```

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Figure 11: CPN100508

```

ctctgattta tggtaattct ttattttcag agccgtcaag tcttttctat tctgttgaat 60
ttcctaataa cgtaagtaat aaacaatcaa aagtcocgcat atg aaa aga cct ttt 115
Met Lys Arg Pro Phe
1 5

ttt acc tat cta tgc atc atc ttc tac gga tct tgt gca tgc tta tct 163
Phe Thr Tyr Leu Cys Ile Ile Phe Tyr Gly Ser Cys Ala Ser Leu Ser
10 15 20

tta cat gca gga etc tct ttc cca gaa gta cgt gga gct acg gct gct 211
Leu His Ala Gly Leu Ser Phe Pro Glu Val Arg Gly Ala Thr Ala Ala
25 30 35

gtt gtc cat gcc gac tct ggg aag gta ttc tat gat aaa gac ata gat 259
Val Val His Ala Asp Ser Gly Lys Val Phe Tyr Asp Lys Asp Ile Asp
Val Val His Ala Asp Ser Gly Lys Val Phe Tyr Asp Lys Asp Ile Asp
40 45 50

gct gta atc tat cct gcc agc atg acg aaa atc gca act gcc etc ttt 307
Ala Val Ile Tyr Pro Ala Ser Met Thr Lys Ile Ala Thr Ala Leu Phe
Ala Val Ile Tyr Pro Ala Ser Met Thr Lys Ile Ala Thr Ala Leu Phe
55 60 65

atc cta aag cac tat ccc aca gtc etc gat act etc atc aaa gtc aaa 355
Ile Leu Lys His Tyr Pro Thr Val Leu Asp Thr Leu Ile Lys Val Lys
Ile Leu Lys His Tyr Pro Thr Val Leu Asp Thr Leu Ile Lys Val Lys
70 75 80 85

caa gat gcg atc gct tcc atc act ccg caa gca aaa aaa caa tca gga 403
Gln Asp Ala Ile Ala Ser Ile Thr Pro Gln Ala Lys Lys Gln Ser Gly
Gln Asp Ala Ile Ala Ser Ile Thr Pro Gln Ala Lys Lys Gln Ser Gly
90 95 100

tat cgt agt cct ccc cac tgg tta gaa act gat gga tct aca ata cag 451
Tyr Arg Ser Pro Pro His Trp Leu Glu Thr Asp Gly Ser Thr Ile Gln
Tyr Arg Ser Pro Pro His Trp Leu Glu Thr Asp Gly Ser Thr Ile Gln
105 110 115

ctc cat ctt cga gaa gag ctt tta ggg tgg gac ctg ttc cac gcc tta 499
Leu His Leu Arg Glu Glu Leu Leu Gly Trp Asp Leu Phe His Ala Leu
Leu His Leu Arg Glu Glu Leu Leu Gly Trp Asp Leu Phe His Ala Leu
120 125 130

ctg gtc tgt tct gct aat gat gct gcg aat gtc tta gct atg gca tgt 547
Leu Val Cys Ser Ala Asn Asp Ala Ala Asn Val Leu Ala Met Ala Cys
Leu Val Cys Ser Ala Asn Asp Ala Ala Asn Val Leu Ala Met Ala Cys
135 140 145

tgc gga tct gta gag aag ttt atg gat aag ctg aac ttc ttc tta aaa 595
Cys Gly Ser Val Glu Lys Phe Met Asp Lys Leu Asn Phe Phe Leu Lys
Cys Gly Ser Val Glu Lys Phe Met Asp Lys Leu Asn Phe Phe Leu Lys
150 155 160 165

gaa gaa atc gcc tgc act cat acc cat ttt aat aat ccc cat ggg tta 643
Glu Glu Ile Gly Cys Thr His Thr His Phe Asn Asn Pro His Gly Leu
Glu Glu Ile Gly Cys Thr His Thr His Phe Asn Asn Pro His Gly Leu
170 175 180

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Fig. 11 (con't)

cat cat ccg aat cac tat act aca acc cgt gat ctt att agc atc atg	691
His His Pro Asn His Tyr Thr Thr Thr Arg Asp Leu Ile Ser Ile Met	
His His Pro Asn His Tyr Thr Thr Thr Arg Asp Leu Ile Ser Ile Met	
185 190 195	
cgt tgc gct ctg aaa gaa cct cca ttt cga ggg gtc atc tcc acg aca	739
Arg Cys Ala Leu Lys Glu Pro Pro Phe Arg Gly Val Ile Ser Thr Thr	
Arg Cys Ala Leu Lys Glu Pro Pro Phe Arg Gly Val Ile Ser Thr Thr	
200 205 210	
agc tat aaa ata ggg gct aca aac ctg cat ggc gaa cgg atc cta tcc	787
Ser Tyr Lys Ile Gly Ala Thr Asn Leu His Gly Glu Arg Ile Leu Ser	
Ser Tyr Lys Ile Gly Ala Thr Asn Leu His Gly Glu Arg Ile Leu Ser	
215 220 225	
cca aca aac aaa ttg ctt ctt cct ggg tct acc tac cac tat ccc cca	835
Pro Thr Asn Lys Leu Leu Leu Pro Gly Ser Thr Tyr His Tyr Pro Pro	
Pro Thr Asn Lys Leu Leu Leu Pro Gly Ser Thr Tyr His Tyr Pro Pro	
230 235 240 245	
gct tta gga ggg aaa aca ggg acc acc aag act gca ggg aaa aat cta	883
Ala Leu Gly Gly Lys Thr Gly Thr Thr Lys Thr Ala Gly Lys Asn Leu	
Ala Leu Gly Gly Lys Thr Gly Thr Thr Lys Thr Ala Gly Lys Asn Leu	
250 255 260	
att atg gct gct gaa aaa aat aac cgc ctc ttg gta acg atc gca acg	931
Ile Met Ala Ala Glu Lys Asn Asn Arg Leu Leu Val Thr Ile Ala Thr	
Ile Met Ala Ala Glu Lys Asn Asn Arg Leu Leu Val Thr Ile Ala Thr	
265 270 275	
ggc tat tgc ggt cct gtg agt gat ctc tac caa gat gtc att gct cta	979
Gly Tyr Ser Gly Pro Val Ser Asp Leu Tyr Gln Asp Val Ile Ala Leu	
Gly Tyr Ser Gly Pro Val Ser Asp Leu Tyr Gln Asp Val Ile Ala Leu	
280 285 290	
tgt gaa acg gta ttt aac gag ccg cta tta aga aaa gag ctc gtc ccc	1027
Cys Glu Thr Val Phe Asn Glu Pro Leu Leu Arg Lys Glu Leu Val Pro	
Cys Glu Thr Val Phe Asn Glu Pro Leu Leu Arg Lys Glu Leu Val Pro	
295 300 305	
ccc tcc gac tgt ctc caa tta gaa ata gcg aat ctt ggg aag ctt tct	1075
Pro Ser Asp Cys Leu Gln Leu Glu Ile Ala Asn Leu Gly Lys Leu Ser	
Pro Ser Asp Cys Leu Gln Leu Glu Ile Ala Asn Leu Gly Lys Leu Ser	
310 315 320 325	
tgc cct ctt cct gag gga ctc tac tat gac ttc tat gcc tcc gaa gat	1123
Cys Pro Leu Pro Glu Gly Leu Tyr Tyr Asp Phe Tyr Ala Ser Glu Asp	
Cys Pro Leu Pro Glu Gly Leu Tyr Tyr Asp Phe Tyr Ala Ser Glu Asp	
330 335 340	
cgc gaa cct ctt tot gta tct ttt att gca cat gcg gac gcc ttc cct	1171
Arg Glu Pro Leu Ser Val Ser Phe Ile Ala His Ala Asp Ala Phe Pro	
Arg Glu Pro Leu Ser Val Ser Phe Ile Ala His Ala Asp Ala Phe Pro	
345 350 355	
att gaa caa gga gat ctt ctt ggt cat tgg gtt ttt tat gac gat gaa	1219
Ile Glu Gln Gly Asp Leu Leu Gly His Trp Val Phe Tyr Asp Asp Glu	
Ile Glu Gln Gly Asp Leu Leu Gly His Trp Val Phe Tyr Asp Asp Glu	
360 365 370	

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Fig. 11 (con't)

ggc aag aaa att tct tcc cag cct ttc tat gcc cct tgt cgt ttt gag	1267
Gly Lys Lys Ile Ser Ser Gln Pro Phe Tyr Ala Pro Cys Arg Phe Glu	
375 380 385	
cgc act atc aag cct tgg aaa ctc tat atg aaa cgt gtc ttc aca tcg	1315
Arg Thr Ile Lys Pro Trp Lys Leu Tyr Met Lys Arg Val Phe Thr Ser	
390 395 400 405	
tat aga acc tat atg tct ata acc atg ctg ctc atg tat ttt cgc atc	1363
Tyr Arg Thr Tyr Met Ser Ile Thr Met Leu Leu Met Tyr Phe Arg Ile	
410 415 420	
cgc aag cac cgc aag tat aaa aat tta aaa cac tat tct aaa atc	1408
Arg Lys His Arg Lys Tyr Lys Asn Leu Lys His Tyr Ser Lys Ile	
425 430 435	
taactttttc ttttaattta taaaaaacca aagggtttatg taagatttgc gcttttcaat	1468
ccaacaagaa tcccttgtgc gcacattact tt	1500



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Fig. 12 (con't)

Tth111II  
 BsiEI  
 PvuI  
 SgfI  
 DpnI  
 Sau3AI  
 BccI  
 AciI  
 Cac8I  
 Hpy178III  
 Tth111II  
 Pfl1108I  
 EcoRV

361 TGC GAT CG CT TCC AT CACT CCG CA AG CAAAAA CA AT CAG GAT AT C G TAG CT CT CCCC A  
 420 ACG CT AG C GA AG GT AG T GAG GCG TT CG T T T T T G T T AG T C C T AT AG C AT CAG GAG GGG T

Hpy178III  
 AceIII  
 TaqI  
 BsrI  
 BstYI  
 Sau3AI  
 MnlI  
 DpnI  
 BccI  
 AlwI  
 MboII  
 BccI  
 AluI  
 CviJI  
 SapI  
 CviJI  
 MboII

421 CTG GT T AG A A A C T G AT G G A C T C A C A G C T C C A C T T T C G A A G A G C T T T T A G G G T G  
 480 G A C C A A C T C T T G A C T A C T A G A T G T T A T G T C G A G G T A G A A G C T C T T C T C G A A A T C C C A C

NlaIV  
 AvaII  
 EcoO109I  
 Psp5II  
 Sau96I  
 BsmFI  
 BsrI  
 BbvI  
 SfaNI  
 Fnu4HI  
 TseI  
 MwoI  
 DdeI  
 AluI  
 CviJI

481 GG A C C T G T T C C A C G C C T A C T G G T C T G T C T G C T A A G A T G C T G C G A A T G T C T T A G C T A T  
 540 C C T G G A C A A G G T G C G G A A T G A C C A G A C A A G A C G A T T A C T A C G A C G C T T A C A G A A T C G A T A

SfcI  
 DpnI  
 BstYI  
 Sau3AI  
 AciI  
 NlaIII  
 NspI  
 AlwI  
 AluI  
 CviJI  
 MboII  
 XmnI  
 MseI  
 BbvI  
 BsgI

541 GG C A T G T T G C G G A T C T G T A G A G A A G T T T A T G G A A A G C T G A A C T T C T T C T T A A A A G A G A  
 600 C C G T A C A C G C C T A G A C A T C T C T C A A A T A C C T A T T C G A C T T G A A G A A G A A T T T C T C T C T

[illegible]

Fig. 12 (cont)

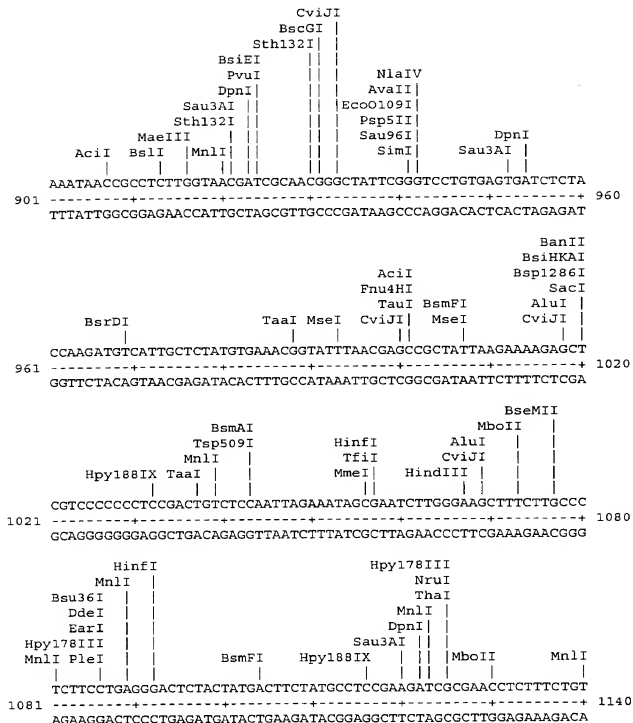


Fig. 12 (cont)

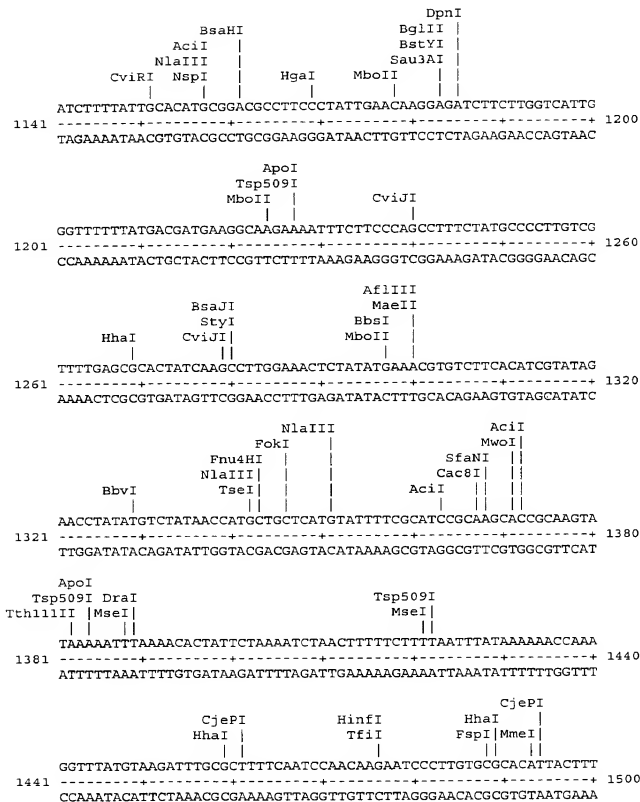


Figure 13: CPN100515-

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aaggagcaaa tggagattgg ccaaatagac gagcaagggt ttgcataaga atagcctttt 60
tcgcaataat aacttgcccta aacgatcttg taaacgactt atg gct tct aat ccc 115
                                     Met Ala Ser Asn Pro
                                     1 5

att tta cag ata gag gat cta tcc ata acc ttg gca aaa caa cgc caa 163
Ile Leu Gln Ile Glu Asp Leu Ser Ile Thr Leu Ala Lys Gln Arg Gln
Ile Leu Gln Ile Glu Asp Leu Ser Ile Thr Leu Ala Lys Gln Arg Gln
                                     10 15 20

cag tac ccc atc gtc caa tct tta tcg ttt act atc aat gaa gga caa 211
Gln Tyr Pro Ile Val Gln Ser Leu Ser Phe Thr Ile Asn Glu Gly Gln
Gln Tyr Pro Ile Val Gln Ser Leu Ser Phe Thr Ile Asn Glu Gly Gln
                                     25 30 35

acc tta gca atc att gga gaa tca gga tca gga aaa tct gtc tct gcg 259
Thr Leu Ala Ile Ile Gly Glu Ser Gly Ser Gly Lys Ser Val Ser Ala
Thr Leu Ala Ile Ile Gly Glu Ser Gly Ser Gly Lys Ser Val Ser Ala
                                     40 45 50

cat gca atc ctt cga tta ctt cct tgc ccc cca ttt tct gtt tct ggc 307
His Ala Ile Leu Arg Leu Leu Pro Cys Pro Pro Phe Ser Val Ser Gly
His Ala Ile Leu Arg Leu Leu Pro Cys Pro Pro Phe Ser Val Ser Gly
                                     55 60 65

cag gtc aac ttc caa ggc cac aac tta ctt acg gct tcg cgc tct ata 355
Gln Val Asn Phe Gln Gly His Asn Leu Leu Thr Ala Ser Arg Ser Ile
Gln Val Asn Phe Gln Gly His Asn Leu Leu Thr Ala Ser Arg Ser Ile
                                     70 75 80 85

caa aaa aag att ata ggg aca gaa att tct atg atc ttt caa aac ccg 403
Gln Lys Lys Ile Ile Gly Thr Glu Ile Ser Met Ile Phe Gln Asn Pro
Gln Lys Lys Ile Ile Gly Thr Glu Ile Ser Met Ile Phe Gln Asn Pro
                                     90 95 100

caa gca tct cta aac ccc gtg ttt act att gaa cag cag ttt cga gaa 451
Gln Ala Ser Leu Asn Pro Val Phe Thr Ile Glu Gln Gln Phe Arg Glu
Gln Ala Ser Leu Asn Pro Val Phe Thr Ile Glu Gln Gln Phe Arg Glu
                                     105 110 115

att att cat acc cac cta gcc tta act gca gaa gtt gct aaa gaa aag 499
Ile Ile His Thr His Leu Ala Leu Thr Ala Glu Val Ala Lys Glu Lys
Ile Ile His Thr His Leu Ala Leu Thr Ala Glu Val Ala Lys Glu Lys
                                     120 125 130

atg tta tac gct ctt gaa gaa aca ggg ttt cat gat ccc agg ctg tgc 547
Met Leu Tyr Ala Leu Glu Glu Thr Gly Phe His Asp Pro Arg Leu Cys
Met Leu Tyr Ala Leu Glu Glu Thr Gly Phe His Asp Pro Arg Leu Cys
                                     135 140 145

ttg aat ctc tac ccc cac caa ctc tct gga ggg atg ctt caa aga att 595
Leu Asn Leu Tyr Pro His Gln Leu Ser Gly Gly Met Leu Gln Arg Ile
Leu Asn Leu Tyr Pro His Gln Leu Ser Gly Gly Met Leu Gln Arg Ile
                                     150 155 160 165

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Fig. 13 (con't)

tgc att gcc atg gcg ctc ctc tgt tct cct aaa ctt ctt att gct gat Cys Ile Ala Met Ala Leu Leu Cys Ser Pro Lys Leu Leu Ile Ala Asp Cys Ile Ala Met Ala Leu Leu Cys Ser Pro Lys Leu Leu Ile Ala Asp	643 170 175 180
gaa cct acg act gct tta gat gtt tct gtt cag tat cag att cta caa Glu Pro Thr Thr Ala Leu Asp Val Ser Val Gln Tyr Gln Ile Leu Gln Glu Pro Thr Thr Ala Leu Asp Val Ser Val Gln Tyr Gln Ile Leu Gln	691 185 190 195
tta cta aaa aca cta cag aaa aaa acg gga atg agc ctt ctt att att Leu Leu Lys Thr Leu Gln Lys Lys Thr Gly Met Ser Leu Leu Ile Ile Leu Leu Lys Thr Leu Gln Lys Lys Thr Gly Met Ser Leu Leu Ile Ile	739 200 205 210
acc cat aat atg gga gtc gtt gca gaa act gct gat gac gtg ctc gtg Thr His Asn Met Gly Val Val Ala Glu Thr Thr Ala Asp Asp Val Leu Val Thr His Asn Met Gly Val Val Ala Glu Thr Ala Asp Asp Val Leu Val	787 215 220 225
ctc tat gca gga cgc atg gta gaa tgt gcc cct gcg gtt caa atg ttc Leu Tyr Ala Gly Arg Met Val Glu Cys Ala Pro Ala Val Gln Met Phe Leu Tyr Ala Gly Arg Met Val Glu Cys Ala Pro Ala Val Gln Met Phe	835 230 235 240 245
cat aat cct tct cat ccc tat acc cga gat ctt tta gca tcc aga ccc His Asn Pro Ser His Pro Tyr Thr Arg Asp Leu Leu Ala Ser Arg Pro His Asn Pro Ser His Pro Tyr Thr Arg Asp Leu Leu Ala Ser Arg Pro	883 250 255 260
tct cta caa ccg caa caa cta ggt tcc ttc aac ccc att cca gga cag Ser Leu Gln Pro Gln Gln Leu Gly Ser Phe Asn Pro Ile Pro Gly Gln Ser Leu Gln Pro Gln Gln Leu Gly Ser Phe Asn Pro Ile Pro Gly Gln	931 265 270 275
ccc cca cac tac acg gcc ttt ccc tcg gga tgt cgc tat cac cct aga Pro Pro His Tyr Thr Ala Phe Pro Ser Gly Cys Arg Tyr His Pro Arg Pro Pro His Tyr Thr Ala Phe Pro Ser Gly Cys Arg Tyr His Pro Arg	979 280 285 290
tgc tca aaa att tta aat cga tgt tct gcg gaa gct cca gaa atc tat Cys Ser Lys Ile Leu Asn Arg Cys Ser Ala Glu Ala Pro Glu Ile Tyr Cys Ser Lys Ile Leu Asn Arg Cys Ser Ala Glu Ala Pro Glu Ile Tyr	1027 295 300 305
ccg gta cgc gaa ggt cac aaa gta agg gtt gcc tgt atg acg act aat Pro Val Arg Glu Gly His Lys Val Arg Val Gly Cys Met Thr Thr Asn Pro Val Arg Glu Gly His Lys Val Arg Val Gly Cys Met Thr Thr Asn	1075 310 315 320 325
ttt ccc caa cct tta att caa gca acc tca tta aca aag cac tat tac Phe Pro Gln Pro Leu Ile Gln Ala Thr Ser Leu Thr Lys His Tyr Tyr Phe Pro Gln Pro Leu Ile Gln Ala Thr Ser Leu Thr Lys His Tyr Tyr	1123 330 335 340

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Fig. 13 (cont)

aag cgt tcc ttt tgg ttt cag gga aag aca att gcc agt cgt cct gtt Lys Arg Ser Phe Trp Phe Gln Gly Lys Thr Ile Ala Ser Arg Pro Val Lys Arg Ser Phe Trp Phe Gln Gly Lys Thr Ile Ala Ser Arg Pro Val	1171
345 350 355	
gac gac gtc tct ttt tca cta tac tcc aga cgt gct gtc gga ctt att Asp Asp Val Ser Phe Ser Leu Tyr Ser Arg Arg Ala Val Gly Leu Ile Asp Asp Val Ser Phe Ser Leu Tyr Ser Arg Arg Ala Val Gly Leu Ile	1219
360 365 370	
gga gaa tct gga tca ggg aaa agt acc ctg gcg tta gct ctc gca ggt Gly Glu Ser Gly Ser Gly Lys Ser Thr Leu Ala Leu Ala Leu Ala Gly Gly Glu Ser Gly Ser Gly Lys Ser Thr Leu Ala Leu Ala Leu Ala Gly	1267
375 380 385	
ctc cta cct ctc acc tct ggg ttc tta act ttt aac ggc acc cca atc Leu Leu Pro Leu Thr Ser Gly Phe Leu Thr Phe Asn Gly Thr Pro Ile Leu Leu Pro Leu Thr Ser Gly Phe Leu Thr Phe Asn Gly Thr Pro Ile	1315
390 395 400 405	
aag ttg cat tct aaa cac gga cgc cat caa tta cga tct caa gta cgg Lys Leu His Ser Lys His Gly Arg His Gln Leu Arg Ser Gln Val Arg Lys Leu His Ser Lys His Gly Arg His Gln Leu Arg Ser Gln Val Arg	1363
410 415 420	
ttg gtc ttt caa aat cca caa gct tca tta aac ccg cga aya act atc Leu Val Phe Gln Asn Pro Gln Ala Ser Leu Asn Pro Arg Lys Thr Ile Leu Val Phe Gln Asn Pro Gln Ala Ser Leu Asn Pro Arg Lys Thr Ile	1411
425 430 435	
cta gat agt tta ggc cac tct ctg ctt tac cat aaa ctc gtc cca aaa Leu Asp Ser Leu Gly His Ser Leu Leu Tyr His Lys Leu Val Pro Lys Leu Asp Ser Leu Gly His Ser Leu Leu Tyr His Lys Leu Val Pro Lys	1459
440 445 450	
gaa aaa gta cta gca acg gta agg gaa tat tta gaa ttg gta ggg tta Glu Lys Val Leu Ala Thr Val Arg Glu Tyr Leu Glu Leu Val Gly Leu Glu Lys Val Leu Ala Thr Val Arg Glu Tyr Leu Glu Leu Val Gly Leu	1507
455 460 465	
tct gag gag tat ttt tat cgt tat cct cac cag ctt tct gga gga caa Ser Glu Glu Tyr Phe Tyr Arg Tyr Pro His Gln Leu Ser Gly Gly Gln Ser Glu Glu Tyr Phe Tyr Arg Tyr Pro His Gln Leu Ser Gly Gly Gln	1555
470 475 480 485	
caa caa cga gtc tct ata gcg aga gcc cta tta gga gtc cct cag tta Gln Gln Arg Val Ser Ile Ala Arg Ala Leu Leu Gly Val Pro Gln Leu Gln Gln Arg Val Ser Ile Ala Arg Ala Leu Leu Gly Val Pro Gln Leu	1603
490 495 500	
att att tgt gac gaa att gtt tct gct cta gat tta tct att caa gca Ile Ile Cys Asp Glu Ile Val Ser Ala Leu Asp Leu Ser Ile Gln Ala Ile Ile Cys Asp Glu Ile Val Ser Ala Leu Asp Leu Ser Ile Gln Ala	1651
505 510 515	
caa att ctg aat atg ctt gcc gag ctg caa aaa aaa ctc agc ctc aca Gln Ile Leu Asn Met Leu Ala Glu Leu Gln Lys Lys Leu Ser Leu Thr Gln Ile Leu Asn Met Leu Ala Glu Leu Gln Lys Lys Leu Ser Leu Thr	1699
520 525 530	

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Fig. 13 (con't)

tat ctc ttc att tcg cat gat ctt gcc gtt gta cgc tcg ttc tgc aca	1747
Tyr Leu Phe Ile Ser His Asp Leu Ala Val Val Arg Ser Phe Cys Thr	
Tyr Leu Phe Ile Ser His Asp Leu Ala Val Val Arg Ser Phe Cys Thr	
535 540 545	
gag gta ttc att atg tat aag ggg caa att gta gaa aaa gga aat aca	1795
Glu Val Phe Ile Met Tyr Lys Gly Gln Ile Val Glu Lys Gly Asn Thr	
Glu Val Phe Ile Met Tyr Lys Gly Gln Ile Val Glu Lys Gly Asn Thr	
550 555 560 565	
aaa cgc att ttt tct gat cca caa cat cct tat acg cgc atg ttg tta	1843
Lys Arg Ile Phe Ser Asp Pro Gln His Pro Tyr Thr Arg Met Leu Leu	
Lys Arg Ile Phe Ser Asp Pro Gln His Pro Tyr Thr Arg Met Leu Leu	
570 575 580	
aat gcc caa ctt cca gag act cct gat caa agg caa tct aaa cct ata	1891
Asn Ala Gln Leu Pro Glu Thr Pro Asp Gln Arg Gln Ser Lys Pro Ile	
Asn Ala Gln Leu Pro Glu Thr Pro Asp Gln Arg Gln	
585 590 595	
ttc caa gaa tat cac aaa gat tct gaa gaa tct tgc tct aca gga tgc	1939
Phe Gln Glu Tyr His Lys Asp Ser Glu Glu Ser Cys Ser Thr Gly Cys	
600 605 610	
tac ttt tac aat cgt tgt cca caa aaa caa gaa gct tgc aag tca gag	1987
Tyr Phe Tyr Asn Arg Cys Pro Gln Lys Gln Glu Ala Cys Lys Ser Glu	
615 620 625	
atc atc cca aat caa gga gac gcg cac cat aca tac cgt tgt atc cat	2035
Ile Ile Pro Asn Gln Gly Asp Ala His His Thr Tyr Arg Cys Ile His	
630 635 640 645	
tgattcgctc tctacgctat tcttaagcta ccattaagga atcccaaggg agagggtctgc	2095
tctat	2100

Figure 14 (RY-40)

Restriction enzyme analysis of CPN 100515

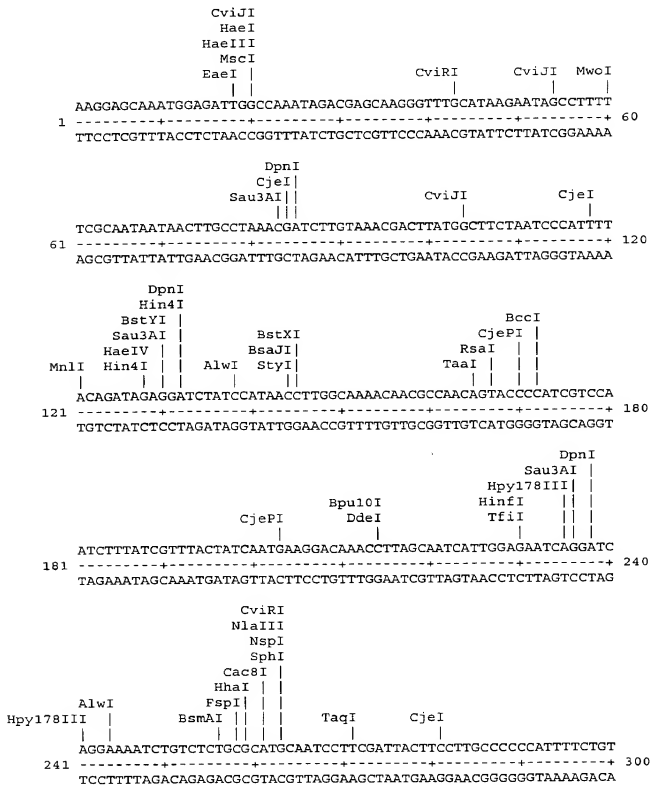


Fig. 14 (cont)

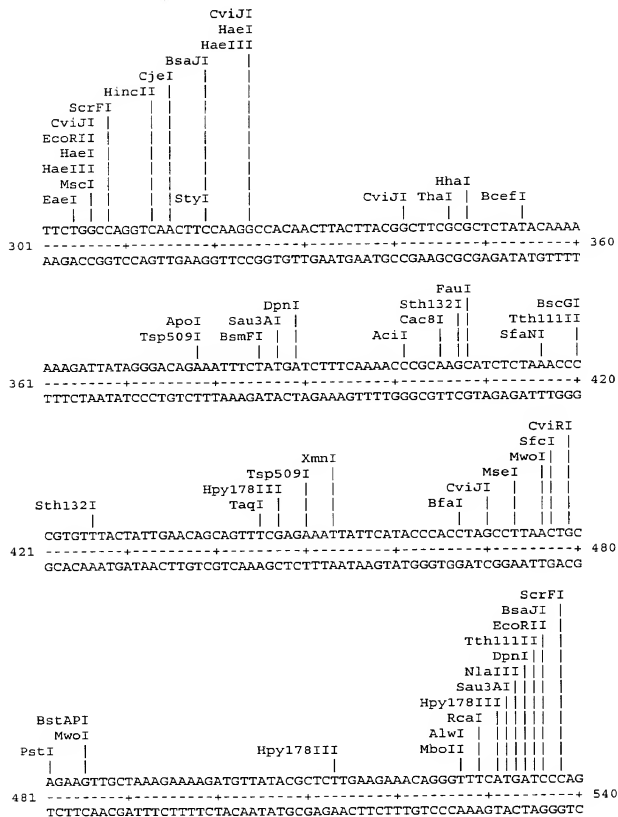


Fig. 14 (con't)

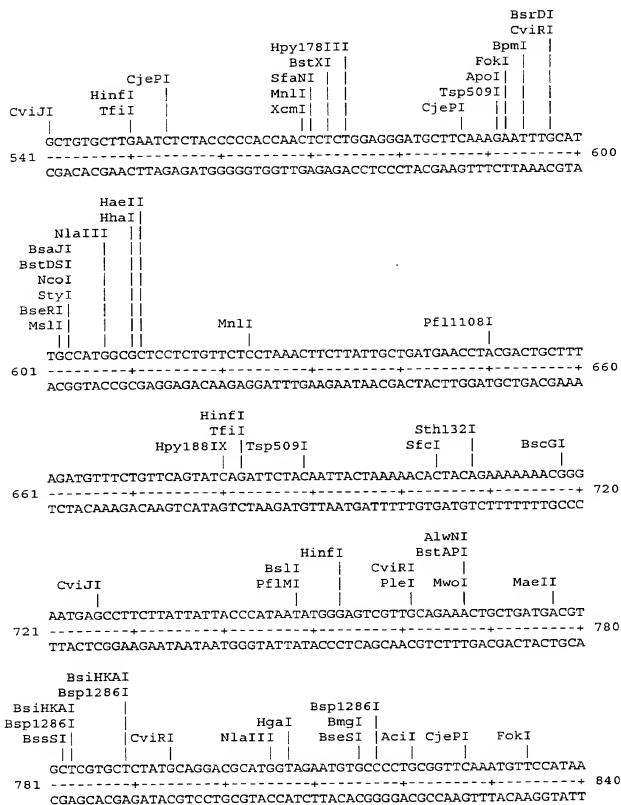
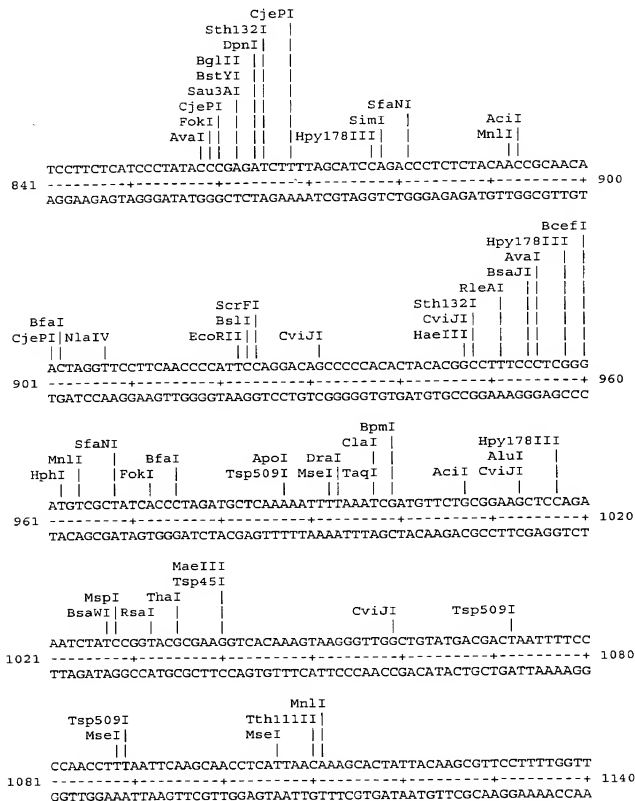


Fig. 14 (cont')



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Fig. 14 (con't)

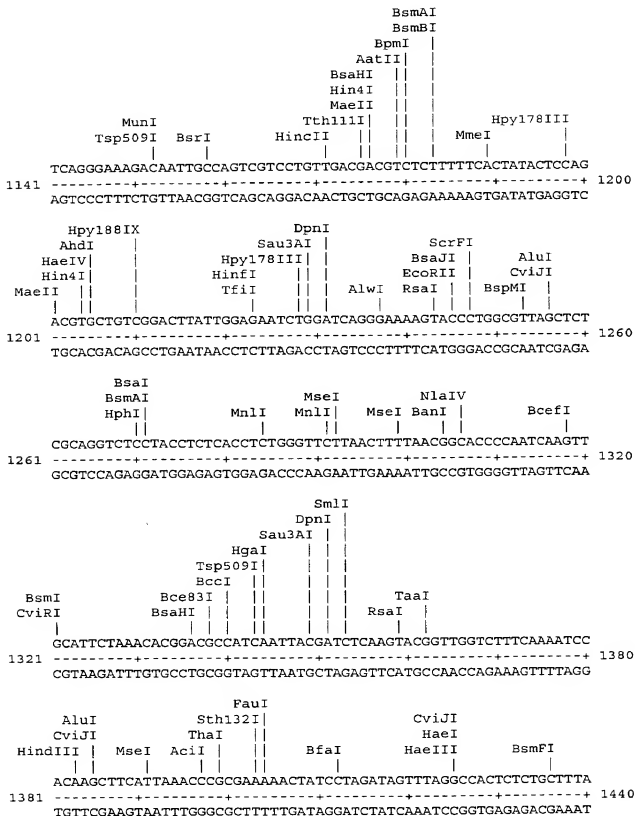




Fig. 14 (cont')

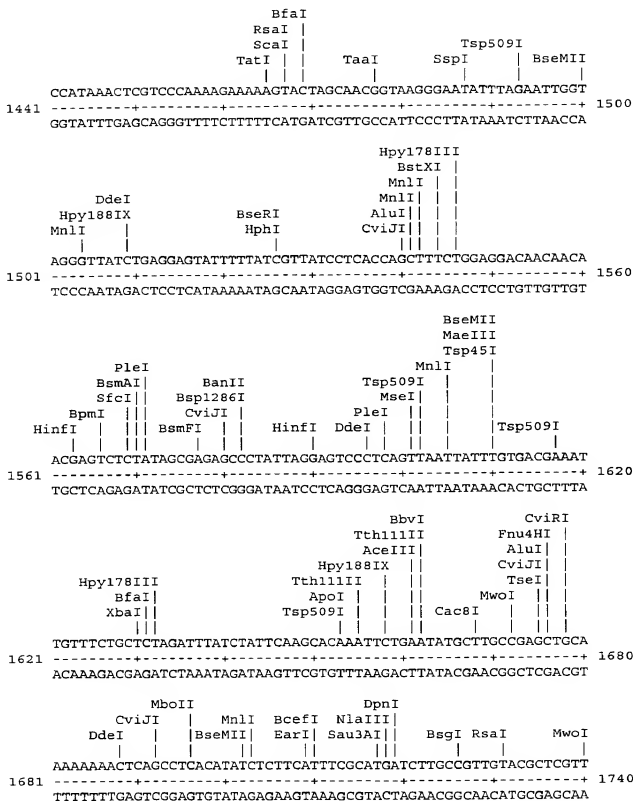
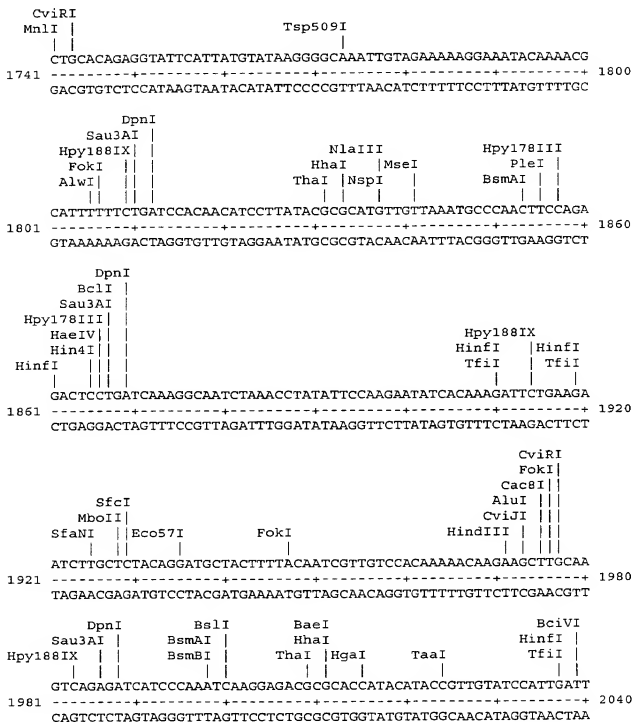


Fig. 14 (cont')



AluI  
 CviI  
 MseI  
 AflII  
 SmaI  
 MnlI  
 BaeI  
 Hin4I  
 MseI  
 TfiI  
 StyI  
 BsaJI  
 MnlI  
 Hin4I

2041  
 CGTCCTCTACGCTATTCTTAAGCTACCATTAAAGGAATCCCAAGGGAGAGGTCTGCTCTAT  
 +-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+  
 GCAGGAGATGCGATAAAGAAATTCGATGGTAATTCCTTAGGGTTCCTCTCCAGACGAGATA 2100

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Figure 15:

```

cgaagagcaa acctccacag ttacagagaa agacgtccaa cctaaaacac aagcaacacc 60
acacgcttcg aagaaaaacg ttgcaagtcg ttcgacctct atg cca gga atc gag 115
Met Pro Gly Ile Glu
1 5

aaa gca gca aca aca gtg gct gta cct caa gac aaa tct gaa gaa gaa 163
Lys Ala Ala Thr Thr Val Ala Val Pro Gln Asp Lys Ser Glu Glu Glu
10 15 20

aaa gtt aaa gag cga ttg aca aag cgg gaa ctt acc tgt gaa gac ctt 211
Lys Val Lys Glu Arg Leu Thr Lys Arg Glu Leu Thr Cys Glu Asp Leu
25 30 35

aaa gat aac ggc tat act gtc aat ttt gaa gac att tct att tta gag 259
Lys Asp Asn Gly Tyr Thr Val Asn Phe Glu Asp Ile Ser Ile Leu Glu
40 45 50

ttg ttg cag ttc gta agt aaa att tct gga acg aac ttt gtc ttt gat 307
Leu Leu Gln Phe Val Ser Lys Ile Ser Gly Thr Asn Phe Val Phe Asp
55 60 65

agc aac gat ttg caa ttc aat gtc acg atc gtt tcc cac gat cct act 355
Ser Asn Asp Leu Gln Phe Asn Val Thr Ile Val Ser His Asp Pro Thr
70 75 80 85

tct gta gat gat tta tct aca atc tta cta caa gtc tta aaa atg cat 403
Ser Val Asp Asp Leu Ser Thr Ile Leu Leu Gln Val Leu Lys Met His
90 95 100

gac ttg aag gtt gtt gaa caa ggc aat aac gtc ctt atc tat cgt aat 451
Asp Leu Lys Val Val Glu Gln Gly Asn Asn Val Leu Ile Tyr Arg Asn
105 110 115

cct cat ctt tct aag cta tcc aca gta gtc aca gac agc tcc tta aaa 499
Pro His Leu Ser Lys Leu Ser Thr Val Val Thr Asp Ser Ser Leu Lys
120 125 130

gaa acg tgt gaa gct gtt gtg gtt acc cga gtg ttc cgt ctt tac agg 547
Glu Thr Cys Glu Ala Val Val Val Thr Arg Val Phe Arg Leu Tyr Arg
135 140 145

cgt cag ccc tct gca gca gta aat att att caa cct tta ctt tcc cat 595
Arg Gln Pro Ser Ala Ala Val Asn Ile Ile Gln Pro Leu Leu Ser His
150 155 160 165

gat gct atc gtt agt gct tca gaa gct act cgt cat gtt atc atc tcg 643
Asp Ala Ile Val Ser Ala Ser Glu Ala Thr Arg His Val Ile Ile Ser
170 175 180

gat att gct ggt aat gtc gat aaa gtc agt gat ttg cta gca gct cta 691
Asp Ile Ala Gly Asn Val Asp Lys Val Ser Asp Leu Leu Ala Ala Leu
185 190 195

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Fig. 15 con't)

gat tgc cca ggc aca tct gtg gac atg act gaa tac gaa gtt aaa tat	739
Asp Cys Pro Gly Thr Ser Val Asp Met Thr Glu Tyr Glu Val Lys Tyr	
200 205 210	
gcc aat ccc gca gct ctt gtt agc tac tgc caa gat gtt ctt ggt act	787
Ala Asn Pro Ala Ala Leu Val Ser Tyr Cys Gln Asp Val Leu Gly Thr	
215 220 225	
ctg gcc gaa gat gat gct ttc caa atg ttc atc caa cct gga acg aac	835
Leu Ala Glu Asp Asp Ala Phe Gln Met Phe Ile Gln Pro Gly Thr Asn	
230 235 240 245	
aaa att ttc gtc gtc tct tca cca cgt ctt gca aat aag gca gag cag	883
Lys Ile Phe Val Val Ser Ser Pro Arg Leu Ala Asn Lys Ala Glu Gln	
250 255 260	
ctc ctg aag tcc tta gat gtc cca gaa atg gca cat acc cta gat gat	931
Leu Leu Lys Ser Leu Asp Val Pro Glu Met Ala His Thr Leu Asp Asp	
265 270 275	
cct gca agt act gcc ttg gct ttg gga gga aca gga acc acg agc cct	979
Pro Ala Ser Thr Ala Leu Ala Leu Gly Gly Thr Gly Thr Thr Ser Pro	
280 285 290	
aag agt ttg cgg ttc ttt atg tac aag ctg aag tat caa aat gga gaa	1027
Lys Ser Leu Arg Phe Phe Met Tyr Lys Leu Lys Tyr Gln Asn Gly Glu	
295 300 305	
gtg att gct aat gcc ctc caa gat atc ggt tac aat cta tat gta acc	1075
Val Ile Ala Asn Ala Leu Gln Asp Ile Gly Tyr Asn Leu Tyr Val Thr	
310 315 320 325	
aca gct atg gac gaa gat ttc att aac act ctc aat agt atc cag tgg	1123
Thr Ala Met Asp Glu Asp Phe Ile Asn Thr Leu Asn Ser Ile Gln Trp	
330 335 340	
tta gag gtc aat aac tcc ata gtt att atc gga aac caa ggg aat gtc	1171
Leu Glu Val Asn Asn Ser Ile Val Ile Ile Gly Asn Gln Gly Asn Val	
345 350 355	
gac aga gtt att ggc ctc tta aac ggt tta gat tta cct cct aaa cag	1219
Asp Arg Val Ile Gly Leu Leu Asn Gly Leu Asp Leu Pro Pro Lys Gln	
360 365 370	
gtt tac atc gaa gtt tta att cta gat acc agc tta gag aaa tcc tgg	1267
Val Tyr Ile Glu Val Leu Ile Leu Asp Thr Ser Leu Glu Lys Ser Trp	
375 380 385	
gac ttt gga gtg caa tgg gta gcc cta ggt gat gaa caa agt aaa gta	1315
Asp Phe Gly Val Gln Trp Val Ala Leu Gly Asp Glu Gln Ser Lys Val	
390 395 400 405	

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Fig. 15 con't)

gct tat gct tct gga cta ttg aat aat act ggc ata gcc aca cct aca	1363
Ala Tyr Ala Ser Gly Leu Leu Asn Asn Thr Gly Ile Ala Thr Pro Thr	
410 415 420	
aaa gca act gtc cct ccc ggc acg cca aat cct ggt tgc atc cct ctt	1411
Lys Ala Thr Val Pro Pro Gly Thr Pro Asn Pro Gly Ser Ile Pro Leu	
425 430 435	
cct acg cca gga caa ttg aca ggg ttc tca gat atg ctg aac tct tgc	1459
Pro Thr Pro Gly Gln Leu Thr Gly Phe Ser Asp Met Leu Asn Ser Ser	
440 445 450	
tca gca ttc ggt cta gga atc atc gga aat gtc cta agt cat aaa ggg	1507
Ser Ala Phe Gly Leu Gly Ile Ile Gly Asn Val Leu Ser His Lys Gly	
455 460 465	
aag tct ttc ctt act ttg gga ggc tta tta agt gcc tta gat caa gat	1555
Lys Ser Phe Leu Thr Leu Gly Gly Leu Leu Ser Ala Leu Asp Gln Asp	
470 475 480 485	
gga gat act gtc att gtc ttg aat cct aga atc atg gct cag gat acg	1603
Gly Asp Thr Val Ile Val Leu Asn Pro Arg Ile Met Ala Gln Asp Thr	
490 495 500	
caa caa gct tgc ttt ttt gta ggg caa acg gtc cct tac caa act atc	1651
Gln Gln Ala Ser Phe Phe Val Gly Gln Thr Val Pro Tyr Gln Thr Ile	
505 510 515	
aaa tac tat atc caa gaa aca gga act gta acg caa aat atc gat tat	1699
Lys Tyr Tyr Ile Gln Glu Thr Gly Thr Val Thr Gln Asn Ile Asp Tyr	
520 525 530	
gaa gat att gga gtg aac ctt gtc gtt acc tct aca gtt gct ccc aac	1747
Glu Asp Ile Gly Val Asn Leu Val Val Thr Ser Thr Val Ala Pro Asn	
535 540 545	
aat gta gtt aca cta caa atc gaa cag acg atc tca gaa tta cat tcc	1795
Asn Val Val Thr Leu Gln Ile Glu Gln Thr Ile Ser Glu Leu His Ser	
550 555 560 565	
gcg tct gga tca cta aca cct gtc aca gat aaa act tat gca gcc aca	1843
Ala Ser Gly Ser Leu Thr Pro Val Thr Asp Lys Thr Tyr Ala Ala Thr	
570 575 580	
cgc tta caa att ccc gac ggt tgt ttc tta gtt atg agt ggg cat atc	1891
Arg Leu Gln Ile Pro Asp Gly Cys Phe Leu Val Met Ser Gly His Ile	
585 590 595	
aga gat aaa act aca aaa gtg gtt tca gga gtg cct ttg cta aac tcc	1939
Arg Asp Lys Thr Thr Lys Val Val Ser Gly Val Pro Leu Leu Asn Ser	
600 605 610	

Fig. 15 con't)

ata cca tta att cgt ggt tta ttt agc cgt acc atc gac caa agg caa	1987
Ile Pro Leu Ile Arg Gly Leu Phe Ser Arg Thr Ile Asp Gln Arg Gln	
615 620 625	
aaa cgc aat atc atg atg ttt att aag cct aag gtg att agt agc ttt	2035
Lys Arg Asn Ile Met Met Phe Ile Lys Pro Lys Val Ile Ser Ser Phe	
630 635 640 645	
gaa gaa ggc act cgt gtt acc aat aag gaa gga tac aga tac aat tgg	2083
Glu Glu Gly Thr Arg Val Thr Asn Lys Glu Gly Tyr Arg Tyr Asn Trp	
650 655 660	
gaa gct gat gaa gga tcc atg caa gtg gcc cct cgc cat gct cct gaa	2131
Glu Ala Asp Glu Gly Ser Met Gln Val Ala Pro Arg His Ala Pro Glu	
665 670 675	
tgc caa gga cct cct tct tta cag gct gaa agt gac ttt aaa ata ata	2179
Cys Gln Gly Pro Pro Ser Leu Gln Ala Glu Ser Asp Phe Lys Ile Ile	
680 685 690	
gaa ata gaa gct cag tagtgggtata taaaagagga agatgatatt ctccgccgtg	2234
Glu Ile Glu Ala Gln	
695	
gaatagcttc tgactctgtt gcattcaggg ggaaagccaa gaagatgtag agtcggccgt	2294
ataact	2300

Figure 16 (RY-41)

Restriction enzyme analysis of CPN100538

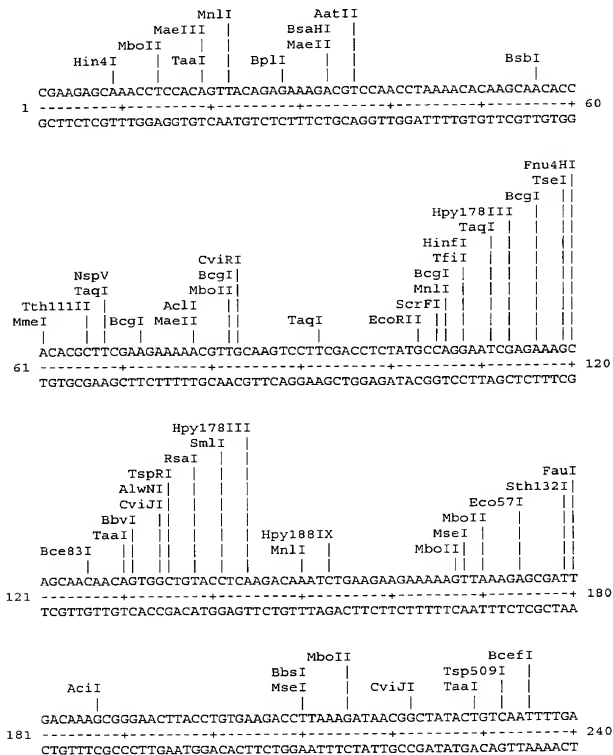




Fig. 16 (con't)

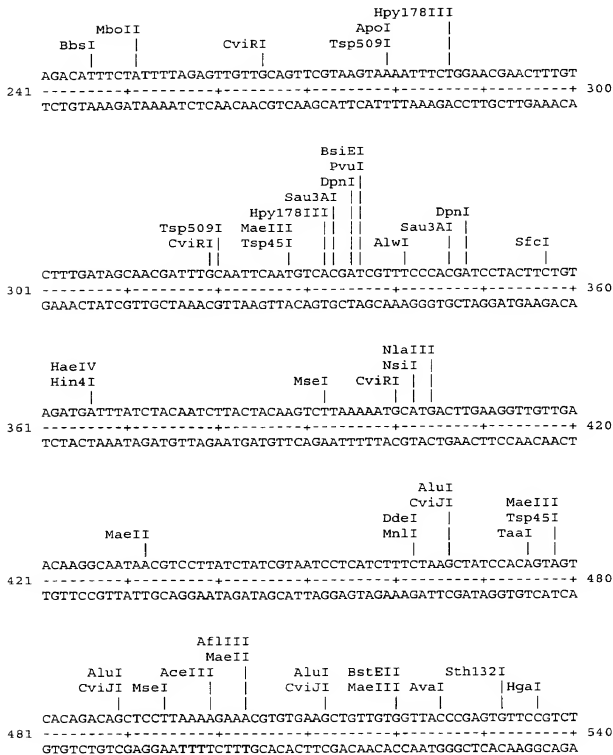






Fig. 16 (con't)

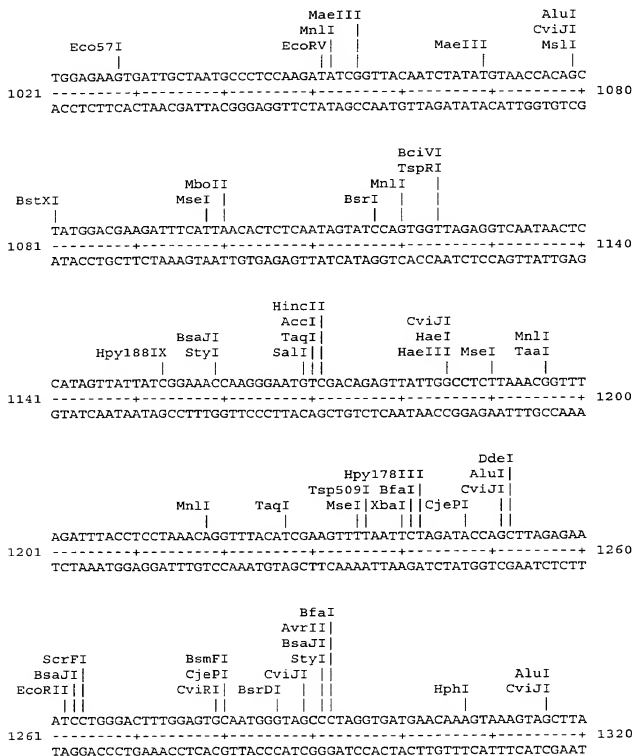
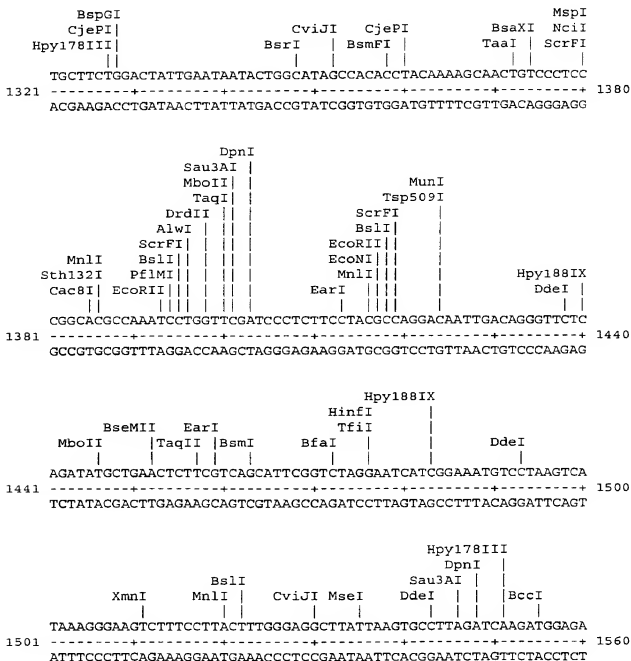


Fig. 16 (con't)



Hpy178III  
 Bpu10I  
 DdeI  
 AluI  
 CviJI  
 BsaXI  
 TaaI  
 HinfI  
 TfiII  
 HinfI  
 TfiII  
 BciVI  
 HindIII  
 BseMII  
 BsmFI  
 Hpn4I  
 Hpy178III  
 BfaI  
 NlaIII  
 TACTGTCATGTCTTGAATCCTAGAATCATCGCTCAGGATACGCAACAAGCTTCGTTTTT  
 1561  
 ATGACAGTAACAGAACTTAGGATCTTAGTACCGAGTCTCTATGCGTTGTTCAAGCAAAAAA  
 NlaIV  
 AvaII  
 Sau96I  
 TaaI  
 MaeIII  
 TaaI  
 AlwNI  
 TGTAGGGCAACGGTCCCTTACCAAACATATCAAATACTATATCCAAGAAACAGGAACTGT  
 1621  
 ACATCCCGTTTGCCAGGGAATGGTTTGATAGTTTATGATATAGGTTCTTTGTCCTTGACA  
 ClaI  
 TaqI  
 MboII  
 MaeIII  
 SfcI  
 BsaXI  
 TaaI  
 MnlI  
 AACGCAAAATATCGATTATGAAGATATTGGAGTGAACCTTGTGTTACCTCTACAGTTGC  
 1681  
 TTGCGTTTTATAGCTAATACTTCTATAACCTCACTTGGACAGCAATGGAGATGTCAACG  
 HgaI  
 Tsp509I  
 Hpy188IX  
 DdeI  
 DpnI  
 Sau3AI  
 MaeIII  
 TaqI  
 AcII  
 BseMII  
 TCCCAACAATGTAGTTACACTACAATTCGAACAGACGATCTCAGAATTACATTCGCGCTC  
 1741  
 AGGGTTGTTACATCAATGTGATGTTTAGCTTGTCGTAGAGTCTTAATGTAAGGCGCAG  
 CviJI  
 Hpy178III  
 Fnu4HI  
 CviRI  
 TseI  
 ApoI  
 Tsp509I  
 BbvI  
 DpnI  
 Sau3AI  
 MaeIII  
 Tsp45I  
 AlwI  
 TGGATCACTAACACCTGTCCAGATAAAACTTATGCAGCCACACGCTTACAAATCCCGA  
 1801  
 ACCTAGTGATTGTGGACAGTGTCTATTTGAATACGTGCGTGTGCGAATGTTTAAAGGCT

PCT/CA99/00992

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SthI32I      DdeI      Hpy188IX      Hpy178III
TaaI  ||      ||      ||      ||
      ||      ||      ||      ||
1861  CGGTGTGTTCTTAGTTATGAGTGGGCATATCAGAGATAAAACTACAAAGTGGTTCAGG
      +-----+-----+-----+-----+-----+-----+-----+-----+
      GCCAACAAAGAATCAATACTACCCGTATAGTCTCTATTTTGATGTTTTCCACCAAGTCC
      1920

      BceI      Bsp509I      MseI      VspI      CviJI      RsaI      BccI      TaqI
      ||      ||      ||      ||      ||      ||      ||      ||
      ||      ||      ||      ||      ||      ||      ||      ||
1921  AGTGCCTTTGCTAAACTCCATACCATTAAATTCGTGGTTTATTAGCCGTACCATCGACCA
      +-----+-----+-----+-----+-----+-----+-----+-----+
      TCACGGAAACGATTTGAGGTATGTAATTAAGCACCAATAAATCGGCATGGTAGCTGGT
      1980

      Bsu36I      DdeI      HphI      AluI      CviJI      MseI      NlaIII      Hpy178III      RcaI
      ||      ||      ||      ||      ||      ||      ||      ||      ||
      ||      ||      ||      ||      ||      ||      ||      ||      ||
1981  AAGGCAAAAACGCAATATCATGATGTTTATTAAAGCCTAAGGTGATTAGTAGCTTTGAAGA
      +-----+-----+-----+-----+-----+-----+-----+-----+
      TTCCGTTTTTGCGTTATAGTACTACAAATAATTCCGATTCCACTAATCATCGAAACTTCT
      2040

      DpnI      NlaIV      BamHI      BstYI      Sau3AI      HaeIV      Hin4I      AlwI      AluI      CviJI      MunI      Tsp509I      BciVI      MaeIII      MboII      BssSI
      ||      ||      ||      ||      ||      ||      ||      ||      ||      ||      ||      ||      ||      ||      ||
      ||      ||      ||      ||      ||      ||      ||      ||      ||      ||      ||      ||      ||      ||      ||
2041  AGGCACCTCGTGTTACCAATAAGGAAGGATACAGATACAATTGGGAAGCTGATGAAGGATC
      +-----+-----+-----+-----+-----+-----+-----+-----+
      TCCGTGAGCACAAATGGTTAATTCCTTCCTATGTCCTATGTTAAACCTTCGACTACTTCCTAG
      2100

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Fig. 16 (con't)

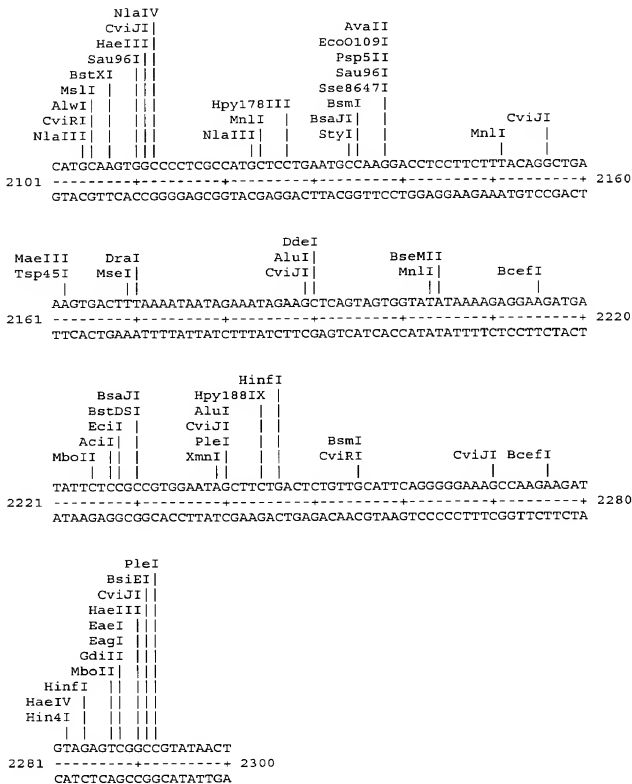




Figure 17: CPN100557

tagcttgaaa	tagcttcctc	caattgtgat	ttctgaagaa	gtataggggg	aaatgtcgaa	60
gagatagctc	tggttttaaag	gaggagggga	aaacgggtta	atg agc aga aaa gac		115
				Met Ser Arg Lys Asp		
				Arg Lys Asp		
				1 5		
aat gag gtt tcc	tta gct cgt tca att	ttt aat ata tta	tcc gga act			163
Asn Glu Val Ser	Leu Ala Arg Ser Ile	Phe Asn Ile Leu	Ser Gly Thr			
Asn Glu Val Ser	Leu Ala Arg Ser Ile	Phe Asn Ile Leu	Ser Gly Thr			
	10	15	20			
ttc tgt agt cgt	att aca ggg ata	ttt cga gaa att	gca atg gca acc			211
Phe Cys Ser Arg	Ile Thr Gly Ile	Phe Arg Glu Ile	Ala Met Ala Thr			
Phe Cys Ser Arg	Ile Thr Gly Ile	Phe Arg Glu Ile	Ala Met Ala Thr			
	25	30	35			
tat ttt gga gct	gat cca att gta	gct gct ttc	tgg tta ggt ttc	cgt		259
Tyr Phe Gly Ala	Asp Pro Ile Val	Ala Ala Phe	Trp Leu Gly Phe	Arg		
Tyr Phe Gly Ala	Asp Pro Ile Val	Ala Ala Phe	Trp Leu Gly Phe	Arg		
	40	45	50			
act gtt ttt ttc	tta aga aaa att	tta gga ggg ctc	att cta gaa caa			307
Thr Val Phe Phe	Leu Arg Lys Ile	Leu Gly Gly Leu	Ile Leu Glu Gln			
Thr Val Phe Phe	Leu Arg Lys Ile	Leu Gly Gly Leu	Ile Leu Glu Gln			
	55	60	65			
gcc ttc atc cct	cat ttt gaa ttt	ctc cgt gct caa	agt ctc gat cgt			355
Ala Phe Ile Pro	His Phe Glu Phe	Leu Arg Ala Gln	Ser Leu Asp Arg			
Ala Phe Ile Pro	His Phe Glu Phe	Leu Arg Ala Gln	Ser Leu Asp Arg			
	70	75	80			
gcg gcg ttt ttt	ttc cga cgc ttt	tct aga ttg att	aaa ggc agc act			403
Ala Ala Phe Phe	Phe Arg Arg Phe	Ser Arg Leu Ile	Lys Gly Ser Thr			
Ala Ala Phe Phe	Phe Arg Arg Phe	Ser Arg Leu Ile	Lys Gly Ser Thr			
	90	95	100			
att ata ttc act	ctg ctt att gaa	gca gta ttg tgg	gta ttc ttc aat			451
Ile Ile Phe Thr	Leu Leu Ile Glu	Ala Val Leu Trp	Val Phe Phe Asn			
Ile Ile Phe Thr	Leu Leu Ile Glu	Ala Val Leu Trp	Val Phe Phe Asn			
	105	110	115			
aac gtt gaa gag	ggg act tac gat	atg att ctc ctt	act atg ata ctc			499
Asn Val Glu Glu	Gly Thr Tyr Asp	Met Ile Leu Leu	Thr Met Ile Leu			
Asn Val Glu Glu	Gly Thr Tyr Asp	Met Ile Leu Leu	Thr Met Ile Leu			
	120	125	130			
ttg ccc tgt ggc	att ttc tta atg	atg tac aat gta	aac ggc gct ttg			547
Leu Pro Cys Gly	Ile Phe Leu Met	Met Tyr Asn Val	Asn Gly Ala Leu			
Leu Pro Cys Gly	Ile Phe Leu Met	Met Tyr Asn Val	Asn Gly Ala Leu			
	135	140	145			
ctt cac tgt gga	aat aag ttt ttc	ggg gtg gga tta	gct ccc gta gtt			595
Leu His Cys Gly	Asn Lys Phe Phe	Gly Val Gly Leu	Ala Pro Val Val			
Leu His Cys Gly	Asn Lys Phe Phe	Gly Val Gly Leu	Ala Pro Val Val			
	150	155	160			
gta aat atc att	tgg att ttc ttt	gtt ata gcg gct	cgt cat tca gat			643
Val Asn Ile Ile	Trp Ile Phe Phe	Val Ile Ala Ala	Arg His Ser Asp			
Val Asn Ile Ile	Trp Ile Phe Phe	Val Ile Ala Ala	Arg His Ser Asp			
	170	175	180			

Title: CHLAMYDIA ANTIGENS AND  
CORRESPONDING DNA FRAGMENTS  
AND USES THEREOF

Inventor(s): Andrew D. MURDIN et al  
DOCKET NO.: 032931/0251

097/830446

WO 00/24765

PCT/CA99/00992

Fig. 17 (con't)

cct aga gag cgt att atc ggt tta tcc gtg gct cta gtt atc ggg ttt Pro Arg Glu Arg Ile Ile Gly Leu Ser Val Ala Leu Val Ile Gly Phe Pro Arg Glu Arg Ile Ile Gly Leu Ser Val Ala Leu Val Ile Gly Phe 185 190 195	691
ttc ttc gaa tgg tta atc acg gtt cct gga gta tgg aaa ttt cta tta Phe Phe Glu Trp Leu Ile Thr Val Pro Gly Val Trp Lys Phe Leu Leu Phe Phe Glu Trp Leu Ile Thr Val Pro Gly Val Trp Lys Phe Leu Leu 200 205 210	739
gaa gcg aag agc cca cct caa gaa cac gat agt gtt cga gct tta tta Glu Ala Lys Ser Pro Pro Gln Glu His Asp Ser Val Arg Ala Leu Leu Glu Ala Lys Ser Pro Pro Gln Glu His Asp Ser Val Arg Ala Leu Leu 215 220 225	787
gct ccc tta tct ttg ggt att tta act tca agc atc ttc cag ctg aac Ala Pro Leu Ser Leu Gly Ile Leu Thr Ser Ser Ile Phe Gln Leu Asn Ala Pro Leu Ser Leu Gly Ile Leu Thr Ser Ser Ile Phe Gln Leu Asn 230 235 240 245	835
ctt ctt tct gat atc tgc ttg gct cgc tat gta cat gaa ata ggc cct Leu Leu Ser Asp Ile Cys Leu Ala Arg Tyr Val His Glu Ile Gly Pro Leu Leu Ser Asp Ile Cys Leu Ala Arg Tyr Val His Glu Ile Gly Pro 250 255 260	883
cta tat ctt atg tac tcc tta aag att tat cag ctc ccc ata cat ctc Leu Tyr Leu Met Tyr Ser Leu Lys Ile Tyr Gln Leu Pro Ile His Leu Leu Tyr Leu Met Tyr Ser Leu Lys Ile Tyr Gln Leu Pro Ile His Leu 265 270 275	931
ttt ggc ttt ggt gtg ttt acc gtt ctc ctc cca gca att tct cgt tgt Phe Gly Phe Gly Val Phe Thr Val Leu Leu Pro Ala Ile Ser Arg Cys Phe Gly Phe Gly Val Phe Thr Val Leu Leu Pro Ala Ile Ser Arg Cys 280 285 290	979
gta cag cga gaa gat cat gag agg gga ttg aaa ctt atg aag ttc gtt Val Gln Arg Glu Asp His Glu Arg Gly Leu Lys Leu Met Lys Phe Val Val Gln Arg Glu Asp His Glu Arg Gly Leu Lys Leu Met Lys Phe Val 295 300 305	1027
ctc acc cta acc atg tcc gta atg atc att atg aca gca ggg cta ttg Leu Thr Leu Thr Met Ser Val Met Ile Ile Met Thr Ala Gly Leu Leu Leu Thr Leu Thr Met Ser Val Met Ile Ile Met Thr Ala Gly Leu Leu 310 315 320 325	1075
ctc tta gct tta cct gga gtc cgt gtc ctt tat gaa cac gga ctt ttc Leu Leu Ala Leu Pro Gly Val Arg Val Leu Tyr Glu His Gly Leu Phe Leu Leu Ala Leu Pro Gly Val Arg Val Leu Tyr Glu His Gly Leu Phe 330 335 340	1123
cct cag agt gct gtc tac gct att gtt cgt gta ttg cga ggt tat ggt Pro Gln Ser Ala Val Tyr Ala Ile Val Arg Val Leu Arg Gly Tyr Gly Pro Gln Ser Ala Val Tyr Ala Ile Val Arg Val Leu Arg Gly Tyr Gly 345 350 355	1171
gcc agt att atc cct atg gcc ttg gct cct tta gtc tct gtt ctt ttt Ala Ser Ile Ile Pro Met Ala Leu Ala Pro Leu Val Ser Val Leu Phe Ala Ser Ile Ile Pro Met Ala Leu Ala Pro Leu Val Ser Val Leu Phe 360 365 370	1219

Title: CHLAMYDIA ANTIGENS AND  
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Inventor(s): Andrew D. MURDIN et al  
DOCKET NO.: 032931/0251

09/830446

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PCT/CA99/00992

Fig. 17 (con't)

tat gca cag cgg cag tat gct gtt ccg ctc ttt ata gga atc ggt acg	1267
Tyr Ala Gln Arg Gln Tyr Ala Val Pro Leu Phe Ile Gly Ile Gly Thr	
Tyr Ala Gln Arg Gln Tyr Ala Val Pro Leu Phe Ile Gly Ile Gly Thr	
375 380 385	
gct ttg gcc aat att gtt tta agc ttg gtt cta ggt cgt tgg gtt tta	1315
Ala Leu Ala Asn Ile Val Leu Ser Leu Val Leu Gly Arg Trp Val Leu	
Ala Leu Ala Asn Ile Val Leu Ser Leu Val Leu Gly Arg Trp Val Leu	
390 395 400 405	
aaa gac gtc tcg ggc att tcc tat gct aca tcc ata act gct tgg gtg	1363
Lys Asp Val Ser Gly Ile Ser Tyr Ala Thr Ser Ile Thr Ala Trp Val	
Lys Asp Val Ser Gly Ile Ser Tyr Ala Thr Ser Ile Thr Ala Trp Val	
410 415 420	
cag tta tat ttc ctc tgg tat tat tct tcg aaa aga ctc cct atg tac	1411
Gln Leu Tyr Phe Leu Trp Tyr Tyr Ser Ser Lys Arg Leu Pro Met Tyr	
Gln Leu Tyr Phe Leu Trp Tyr Tyr Ser Ser Lys Arg Leu Pro Met Tyr	
425 430 435	
tct aag tta ctt tgg gag agc atc cgg cgt tcc ata aaa gct atg gga	1459
Ser Lys Leu Leu Trp Glu Ser Ile Arg Arg Ser Ile Lys Val Met Gly	
Ser Lys Leu Leu Trp Glu Ser Ile Arg Arg Ser Ile Lys Val Met Gly	
440 445 450	
acc act atg ctt gct tgt atg att act cta ggc tta aat atc ctt acg	1507
Thr Thr Met Leu Ala Cys Met Ile Thr Leu Gly Leu Asn Ile Leu Thr	
Thr Thr Met Leu Ala Cys Met Ile Thr Leu Gly Leu Asn Ile Leu Thr	
455 460 465	
caa act aca tat gta att ttc tta aac ccc ctc aca cca ctt gct tgg	1555
Gln Thr Thr Tyr Val Ile Phe Leu Asn Pro Leu Thr Pro Leu Ala Trp	
Gln Thr Thr Tyr Val Ile Phe Leu Asn Pro Leu Thr Pro Leu Ala Trp	
470 475 480 485	
ccc tta tcc tcc ata acg gct caa gca att gct ttt tta tct gag agc	1603
Pro Leu Ser Ser Ile Thr Ala Gln Ala Ile Ala Phe Leu Ser Glu Ser	
Pro Leu Ser Ser Ile Thr Ala Gln Ala Ile Ala Phe Leu Ser Glu Ser	
490 495 500	
tgc att ttc ttg gct ttt ttg ttt ggt ttt gca aaa ctg ctt cga gta	1651
Cys Ile Phe Leu Ala Phe Leu Phe Gly Phe Ala Lys Leu Leu Arg Val	
Cys Ile Phe Leu Ala Phe Leu Phe Gly Phe Ala Lys Leu Leu Arg Val	
505 510 515	
gaa gat ctt att aat ttg gct tct ttt gaa tac tgg cgt ggg caa cgg	1699
Glu Asp Leu Ile Asn Leu Ala Ser Phe Glu Tyr Trp Arg Gly Gln Arg	
Glu Asp Leu Ile Asn Leu Ala Ser Phe Glu Tyr Trp Arg Gly Gln Arg	
520 525 530	
ggg ctt ttg caa aga caa cac gtg atg caa gac act caa aat	1741
Gly Leu Leu Gln Arg Gln His Val Met Gln Asp Thr Gln Asn	
Gly Leu Leu Gln	
535 540 545	
taatcatggt tggtttctgt agctcagtcg ctttctttta gctttaagtt ttgatagcct	1801
gcttggtctt ctgtttctac acttaatat gatactaagg atactatgaa aaaacaggta	1861
tatcaatggt tagcgagtggt gggtctttta gcgctgaca	1900

Figure 18 (RY-43)

### Restriction enzyme analysis of CPN100557

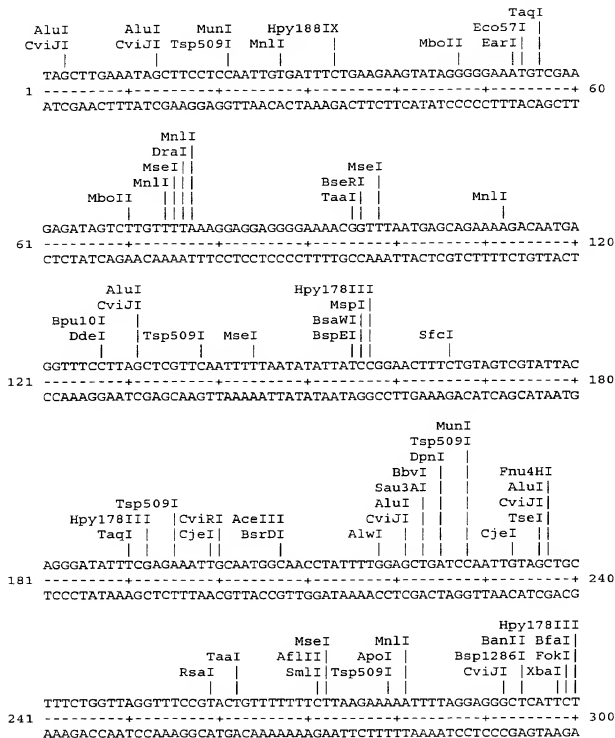


Fig. 18 (cont')

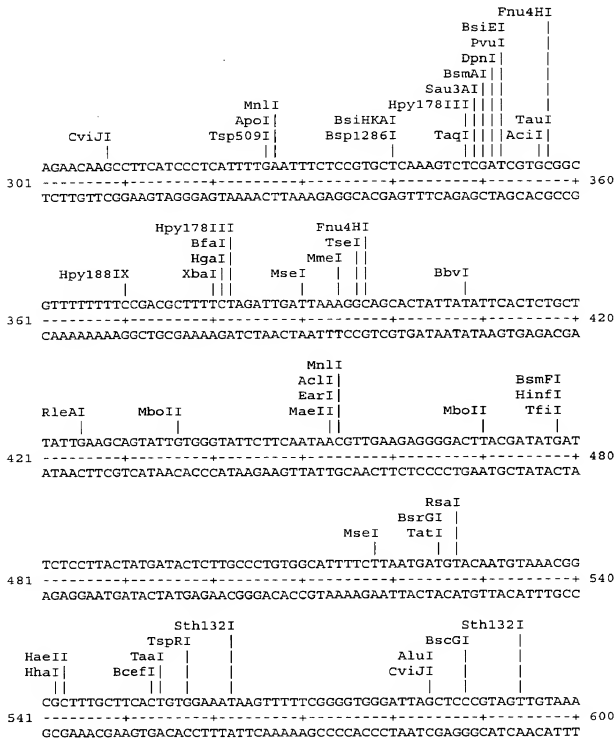


Fig. 18 (con't)

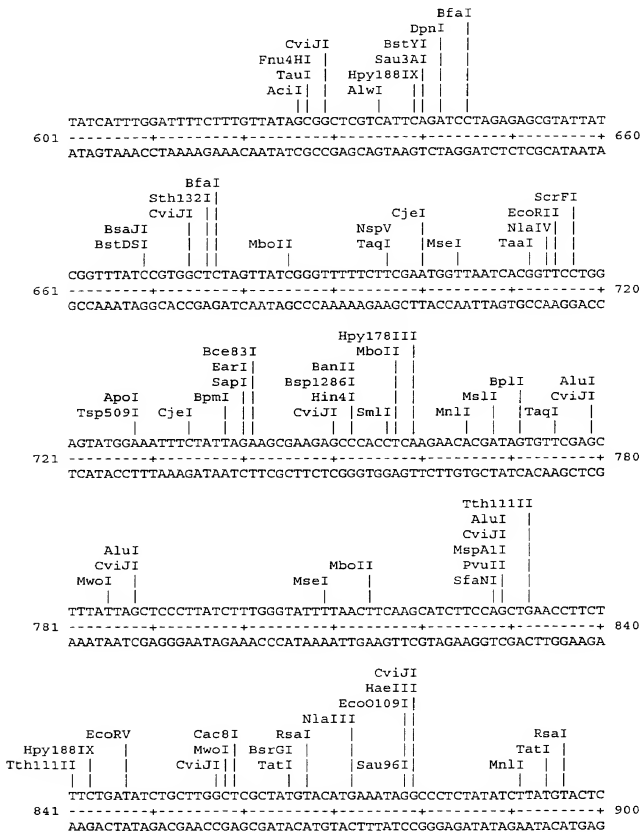


Fig. 18 (con't)

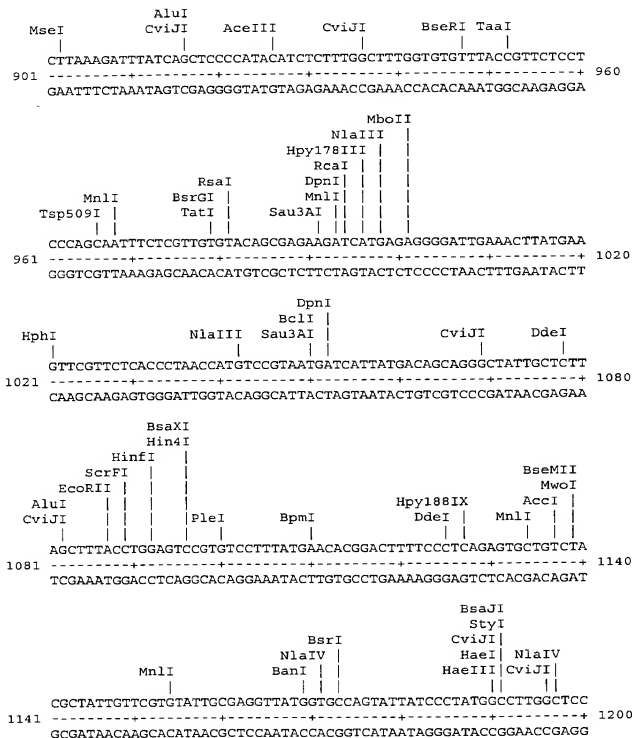


Fig. 18 (con't)

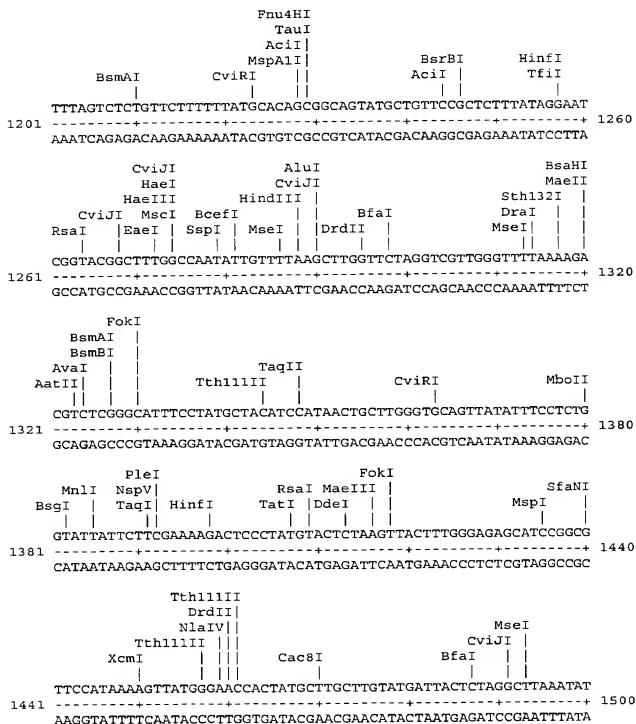
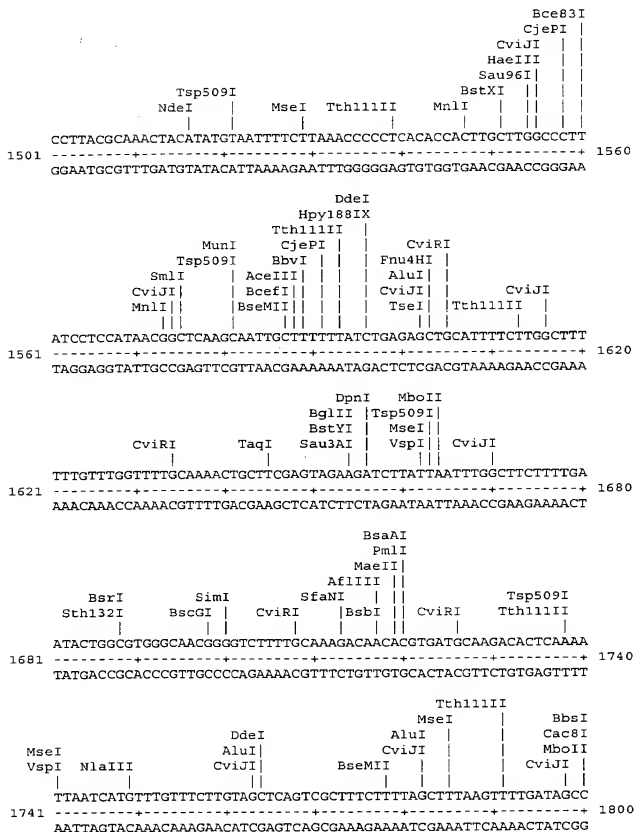


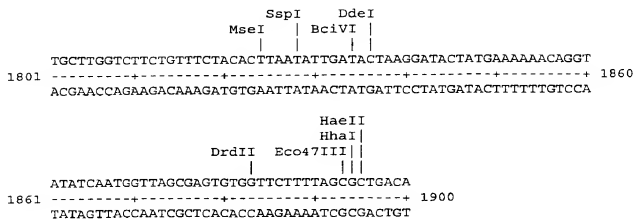


Fig. 18 (con't)



WO 00/24765

Fig. 18 (con't)



Title: CHLAMYDIA ANTIGENS AND  
CORRESPONDING DNA FRAGMENTS  
AND USES THEREOF

Inventor(s): Andrew D. MURDIN et al  
DOCKET NO.: 032931/0251

09/830446

PCT/CA99/00992

WO 00/24765

Figure 19: CPN100622

```
tctcaagagt aaccttatcc ttagattatt cagctcaagt ctctctgtca actgtaggtc 60
aataccttaa agctgagagt cattgcacat ttttaaccaca atg aaa aca tca agg 115
                                         Met Lys Thr Ser Arg
                                         1                               5

aat aaa cag tgc aaa ata aca gat ccc tta agt aaa tct tcc ttc ttt 163
Asn Lys Gln Cys Lys Ile Thr Asp Pro Leu Ser Lys Ser Ser Phe Phe
                      10                               15                               20

gtt gga gcc tta att tta ggt aaa act aca ata ctc ctt aat gcg act 211
Val Gly Ala Leu Ile Leu Gly Lys Thr Thr Ile Leu Leu Asn Ala Thr
                      25                               30                               35

ccg ttg tct gac tat ttt gat aat caa gca aat caa ctc aca aca ctc 259
Pro Leu Ser Asp Tyr Phe Asp Asn Gln Ala Asn Gln Leu Thr Thr Leu
                      40                               45                               50

ttc cct cta att gat act ctt act aac atg act ccc tac tct cat aga 307
Phe Pro Leu Ile Asp Thr Leu Thr Asn Met Thr Pro Tyr Ser His Arg
                      55                               60                               65

gca aca ctt ttt gga gtt agg gat gac act aac caa gac att gtc ctc 355
Ala Thr Leu Phe Gly Val Arg Asp Asp Thr Asn Gln Asp Ile Val Leu
                      70                               75                               80                               85

gat cac cag aat tcc ata gaa agc tgg ttc gaa aac ttc tct caa gac 403
Asp His Gln Asn Ser Ile Glu Ser Trp Phe Glu Asn Phe Ser Gln Asp
                      90                               95                               100

ggc ggt gct ctc tct tgc aaa tca ctt gcc ata acg aat aca aaa aac 451
Gly Gly Ala Leu Ser Cys Lys Ser Leu Ala Ile Thr Asn Thr Lys Asn
                      105                               110                               115

caa att ctt ttc cta aat agc ttt gct att aaa aga gct ggt gcg atg 499
Gln Ile Leu Phe Leu Asn Ser Phe Ala Ile Lys Arg Ala Gly Ala Met
                      120                               125                               130

tat gtt gat ggt aat ttc gat ctt tct gag aat cat ggt tcc atc att 547
Tyr Val Asp Gly Asn Phe Asp Leu Ser Glu Asn His Gly Ser Ile Ile
                      135                               140                               145

ttc tct ggg aat tta agc ttt cct aat gca agt aat ttc gct gat act 595
Phe Ser Gly Asn Leu Ser Phe Pro Asn Ala Ser Asn Phe Ala Asp Thr
                      150                               155                               160                               165

tgt aca ggg gga gct gtt tta tgt tcy aaa aat gtt aca atc tca aaa 643
Cys Thr Gly Gly Ala Val Leu Cys Ser Lys Asn Val Thr Ile Ser Lys
                      170                               175                               180

aat caa gga acc gca tac ttc att aac aac aag gca aaa tct tca gga 691
Asn Gln Gly Thr Ala Tyr Phe Ile Asn Asn Lys Ala Lys Ser Ser Gly
                      185                               190                               195
```

Title: CHLAMYDIA ANTIGENS AND  
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097830446

WO 00/24765

Inventor(s): Andrew D. MURDIN et al  
DOCKET NO.: 032931/0251

PCT/CA99/00992

Fig. 19 (con't)

gga gca atc caa gct gca atc ata aac att aag gac aac act ggc cct Gly Ala Ile Gln Ala Ala Ile Ile Asn Ile Lys Asp Asn Thr Gly Pro Gly Ala Ile Gln Ala Ala Ile Ile Asn Ile Lys Asp Asn Thr Gly Pro 200 205 210	739
tgc ctg ttt ttt aat aat gct gca ggc gga aca gcg ggg ggc gcg ttg Cys Leu Phe Phe Asn Asn Ala Ala Gly Gly Thr Ala Gly Gly Ala Leu Cys Leu Phe Phe Asn Asn Ala Ala Gly Gly Thr Ala Gly Gly Ala Leu 215 220 225	787
ttc gct aat gct tgt aga att gag aat aat tct cag cct atc tat ttt Phe Ala Asn Ala Cys Arg Ile Glu Asn Asn Ser Gln Pro Ile Tyr Phe Phe Ala Asn Ala Cys Arg Ile Glu Asn Asn Ser Gln Pro Ile Tyr Phe 230 235 240 245	835
ttg aat aac caa tca ggt ctg ggt ggt gca ata aga gta cat caa gag Leu Asn Asn Gln Ser Gly Leu Gly Gly Ala Ile Arg Val His Gln Glu Leu Asn Asn Gln Ser Gly Leu Gly Gly Ala Ile Arg Val His Gln Glu 250 255 260	883
tgc att ctt aca aag aat acc ggt tct gtg atc ttc aac aat aat ttt Cys Ile Leu Thr Lys Asn Thr Gly Ser Val Ile Phe Asn Asn Asn Phe Cys Ile Leu Thr Lys Asn Thr Gly Ser Val Ile Phe Asn Asn Asn Phe 265 270 275	931
gcc atg gaa gcg gac atc tct gct aac cat tcc tct gga ggg gct atc Ala Met Glu Ala Asp Ile Ser Ala Asn His Ser Ser Gly Gly Ala Ile Ala Met Glu Ala Asp Ile Ser Ala Asn His Ser Ser Gly Gly Ala Ile 280 285 290	979
tat tgc att agt tgt tct ata aaa gac aac cca gga att gca gcc ttc Tyr Cys Ile Ser Cys Ser Ile Lys Asp Asn Pro Gly Ile Ala Ala Phe Tyr Cys Ile Ser Cys Ser Ile Lys Asp Asn Pro Gly Ile Ala Ala Phe 295 300 305	1027
gat aat aat act gca gca cga gat gga ggt gct atc tgt aca caa tct Asp Asn Asn Thr Ala Ala Arg Asp Gly Gly Ala Ile Cys Thr Gln Ser Asp Asn Asn Thr Ala Ala Arg Asp Gly Gly Ala Ile Cys Thr Gln Ser 310 315 320 325	1075
cta act ata caa gac agt ggt ccc gtc tat ttc aca aac aat cag gga Leu Thr Ile Gln Asp Ser Gly Pro Val Tyr Phe Thr Asn Asn Gln Gly Leu Thr Ile Gln Asp Ser Gly Pro Val Tyr Phe Thr Asn Asn Gln Gly 330 335 340	1123
act tgg ggc ggc gct atc atg ctc cgt caa gat ggt gca tgc act tta Thr Trp Gly Gly Ala Ile Met Leu Arg Gln Asp Gly Ala Cys Thr Leu Thr Trp Gly Gly Ala Ile Met Leu Arg Gln Asp Gly Ala Cys Thr Leu 345 350 355	1171
ttt gct gat cag gga gat att att ttt tat aat aat aga cac ttc aaa Phe Ala Asp Gln Gly Asp Ile Ile Phe Tyr Asn Asn Arg His Phe Lys Phe Ala Asp Gln Gly Asp Ile Ile Phe Tyr Asn Asn Arg His Phe Lys 360 365 370	1219
gat act ttc agc aat cat gtt tct gta aac tgc acg cgt aat gtc tca Asp Thr Phe Ser Asn His Val Ser Val Asn Cys Thr Arg Asn Val Ser Asp Thr Phe Ser Asn His Val Ser Val Asn Cys Thr Arg Asn Val Ser 375 380 385	1267

Fig. 19 (con't)

tta	aca	gtt	gga	gca	agt	caa	ggg	cat	tct	gct	acc	ttc	tat	gat	ccc	1315
Leu	Thr	Val	Gly	Ala	Ser	Gln	Gly	His	Ser	Ala	Thr	Phe	Tyr	Asp	Pro	
Leu	Thr	Val	Gly	Ala	Ser	Gln	Gly	His	Ser	Ala	Thr	Phe	Tyr	Asp	Pro	
390					395					400					405	
ata	cta	caa	aga	tat	act	ata	caa	aac	tct	atc	caa	aaa	ttt	aat	cct	1363
Ile	Leu	Gln	Arg	Tyr	Thr	Ile	Gln	Asn	Ser	Ile	Gln	Lys	Phe	Asn	Pro	
Ile	Leu	Gln	Arg	Tyr	Thr	Ile	Gln	Asn	Ser	Ile	Gln	Lys	Phe	Asn	Pro	
				410					415					420		
aat	cca	gaa	cac	ctc	gga	act	atc	ttg	ttc	tcc	tca	aca	tat	att	cgg	1411
Asn	Pro	Glu	His	Leu	Gly	Thr	Ile	Leu	Phe	Ser	Ser	Thr	Tyr	Ile	Pro	
Asn	Pro	Glu	His	Leu	Gly	Thr	Ile	Leu	Phe	Ser	Ser	Thr	Tyr	Ile	Pro	
			425					430					435			
gat	aca	tcg	act	tct	cgt	gat	gac	ttc	att	tca	cat	ttc	aga	aac	cac	1459
Asp	Thr	Ser	Thr	Ser	Arg	Asp	Asp	Phe	Ile	Ser	His	Phe	Arg	Asn	His	
Asp	Thr	Ser	Thr	Ser	Arg	Asp	Asp	Phe	Ile	Ser	His	Phe	Arg	Asn	His	
			440				445					450				
att	gga	ctg	tac	aac	ggc	aca	ctc	gct	ctt	gaa	gat	cga	gca	gag	tgg	1507
Ile	Gly	Leu	Tyr	Asn	Gly	Thr	Leu	Ala	Leu	Glu	Asp	Arg	Ala	Glu	Trp	
Ile	Gly	Leu	Tyr	Asn	Gly	Thr	Leu	Ala	Leu	Glu	Asp	Arg	Ala	Glu	Trp	
			455			460						465				
aaa	gtc	tat	aaa	ttt	gat	caa	ttt	ggg	ggg	act	cta	cgg	tta	ggc	agt	1555
Lys	Val	Tyr	Lys	Phe	Asp	Gln	Phe	Gly	Gly	Thr	Leu	Arg	Leu	Gly	Ser	
Lys	Val	Tyr	Lys	Phe	Asp	Gln	Phe	Gly	Gly	Thr	Leu	Arg	Leu	Gly	Ser	
470					475					480					485	
aga	gct	gtg	ttt	tct	aca	aca	gac	gaa	gaa	caa	agt	agc	agt	agt	gtg	1603
Arg	Ala	Val	Phe	Ser	Thr	Thr	Thr	Asp	Glu	Gln	Ser	Ser	Ser	Ser	Val	
Arg	Ala	Val	Phe	Ser	Thr	Thr	Thr	Asp	Glu	Gln	Ser	Ser	Ser	Ser	Val	
				490						495					500	
ggg	tct	gta	att	aac	atc	aat	aac	ctt	gca	att	aac	ctt	ccc	tct	atc	1651
Gly	Ser	Val	Ile	Asn	Ile	Asn	Asn	Leu	Ala	Ile	Asn	Leu	Pro	Ser	Ile	
Gly	Ser	Val	Ile	Asn	Ile	Asn	Asn	Leu	Ala	Ile	Asn	Leu	Pro	Ser	Ile	
			505					510					515			
tta	ggc	aac	aga	gtt	gct	ccc	aag	cta	tgq	att	cgc	ccc	aca	ggg	tca	1699
Leu	Gly	Asn	Arg	Val	Ala	Pro	Lys	Leu	Trp	Ile	Arg	Pro	Thr	Gly	Ser	
Leu	Gly	Asn	Arg	Val	Ala	Pro	Lys	Leu	Trp	Ile	Arg	Pro	Thr	Gly	Ser	
			520				525					530				
tca	gca	ccc	tat	agc	gaa	gat	aat	aac	cct	ata	atc	aat	ctc	tca	gga	1747
Ser	Ala	Pro	Tyr	Ser	Glu	Asp	Asn	Asn	Pro	Ile	Ile	Asn	Leu	Ser	Gly	
Ser	Ala	Pro	Tyr	Ser	Glu	Asp	Asn	Asn	Pro	Ile	Ile	Asn	Leu	Ser	Gly	
			535			540					545					
cct	ttg	agc	cta	ctg	gat	gac	gag	aac	cta	gat	ccc	tat	gat	act	gca	1795
Pro	Leu	Ser	Leu	Leu	Asp	Asp	Glu	Asn	Leu	Asp	Pro	Tyr	Asp	Thr	Ala	
Pro	Leu	Ser	Leu	Leu	Asp	Asp	Glu	Asn	Leu	Asp	Pro	Tyr	Asp	Thr	Ala	
			550			555				560					565	
gac	ctt	ggc	caa	cct	atc	gca	gaa	gtt	cct	ctt	ctg	tat	ctc	tta	gac	1843
Asp	Leu	Ala	Gln	Pro	Ile	Ala	Glu	Val	Pro	Leu	Leu	Tyr	Leu	Leu	Asp	
Asp	Leu	Ala	Gln	Pro	Ile	Ala	Glu	Val	Pro	Leu	Leu	Tyr	Leu	Leu	Asp	
				570					575					580		

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Inventor(s): Andrew D. MURDIN et al  
DOCKET NO.: 032931/0251

WO 00/24765

PCT/CA99/00992

Fig. 19 (con't)

tac	agc	aac	cac	cat	atc	aaa	gca	tct	gga	tat	tct	gga	aaa	ata	caa	2467
Tyr	Ser	Asn	His	His	Ile	Lys	Ala	Ser	Gly	Tyr	Ser	Gly	Lys	Ile	Gln	
Tyr	Ser	Asn	His	His	Ile	Lys	Ala	Ser	Gly	Tyr	Ser	Gly	Lys	Ile	Gln	
	775					780					785					
acg	gaa	ggc	aaa	tgt	tat	agt	acg	aca	tta	ggg	gcg	ctc	ctc	tct	tgc	2515
Thr	Glu	Gly	Lys	Cys	Tyr	Ser	Thr	Thr	Leu	Gly	Ala	Ala	Ala	Leu	Ser	Cys
Thr	Glu	Gly	Lys	Cys	Tyr	Ser	Thr	Thr	Leu	Gly	Ala	Ala	Ala	Leu	Ser	Cys
	790				795					800					805	
tct	cta	tct	cta	caa	tgg	cga	tca	cga	ccc	ctc	cac	ttc	act	ccc	ttt	2563
Ser	Leu	Ser	Leu	Gln	Trp	Arg	Ser	Arg	Pro	Leu	His	Phe	Thr	Pro	Phe	
Ser	Leu	Ser	Leu	Gln	Trp	Arg	Ser	Arg	Pro	Leu	His	Phe	Thr	Pro	Phe	
				810					815					820		
atc	caa	gca	att	gcc	gtt	cgt	tct	aat	caa	act	gcg	ttt	caa	gaa	agt	2611
Ile	Gln	Ala	Ile	Ala	Val	Arg	Ser	Asn	Gln	Thr	Ala	Phe	Gln	Glu	Ser	
Ile	Gln	Ala	Ile	Ala	Val	Arg	Ser	Asn	Gln	Thr	Ala	Phe	Gln	Glu	Ser	
				825					830					835		
gga	gat	aaa	gct	aga	aaa	ttt	tct	gtt	cat	aaa	ccc	tta	tat	aac	ctg	2659
Gly	Asp	Lys	Ala	Arg	Lys	Phe	Ser	Val	His	Lys	Pro	Leu	Tyr	Asn	Leu	
Gly	Asp	Lys	Ala	Arg	Lys	Phe	Ser	Val	His	Lys	Pro	Leu	Tyr	Asn	Leu	
				840					845					850		
aca	gtc	ccc	ctg	gga	att	cag	agc	gct	tgg	gaa	tcc	aag	ttc	cgt	ctt	2707
Thr	Val	Pro	Leu	Gly	Ile	Gln	Ser	Ala	Trp	Glu	Ser	Lys	Phe	Arg	Leu	
Thr	Val	Pro	Leu	Gly	Ile	Gln	Ser	Ala	Trp	Glu	Ser	Lys	Phe	Arg	Leu	
				855					860					865		
ccc	acc	tat	tgg	aac	ata	gag	ctt	gct	tat	cag	ccc	gtc	ctc	tac	caa	2755
Pro	Thr	Tyr	Trp	Asn	Ile	Glu	Leu	Ala	Tyr	Gln	Pro	Val	Leu	Tyr	Gln	
Pro	Thr	Tyr	Trp	Asn	Ile	Glu	Leu	Ala	Tyr	Gln	Pro	Val	Leu	Tyr	Gln	
				870					875					880		885
caa	aat	ccc	gag	atc	aac	gtg	agt	cta	gaa	tct	agt	gga	tcg	tca	tgg	2803
Gln	Asn	Pro	Glu	Ile	Asn	Val	Ser	Leu	Glu	Ser	Ser	Gly	Ser	Ser	Trp	
Gln	Asn	Pro	Glu	Ile	Asn	Val	Ser	Leu	Glu	Ser	Ser	Gly	Ser	Ser	Trp	
				890					895					900		
ctc	cta	tca	gga	acc	acc	ctt	gct	cgc	aat	gcc	att	gct	ttt	aaa	gga	2851
Leu	Leu	Ser	Gly	Thr	Thr	Leu	Ala	Arg	Asn	Ala	Ile	Ala	Phe	Lys	Gly	
Leu	Leu	Ser	Gly	Thr	Thr	Leu	Ala	Arg	Asn	Ala	Ile	Ala	Phe	Lys	Gly	
				905					910					915		
aga	aac	caa	att	ttt	atc	ttc	ccc	aaa	ctt	tcg	gtg	ttc	tta	gac	tat	2999
Arg	Asn	Gln	Ile	Phe	Ile	Phe	Pro	Lys	Leu	Ser	Val	Phe	Leu	Asp	Tyr	
Arg	Asn	Gln	Ile	Phe	Ile	Phe	Pro	Lys	Leu	Ser	Val	Phe	Leu	Asp	Tyr	
				920					925					930		
caa	ggc	tcg	gta	tcc	tca	tca	acg	acg	aca	cat	tac	ctt	cac	gca	gga	2947
Gln	Gly	Ser	Val	Ser	Ser	Ser	Thr	Thr	Thr	His	Tyr	Leu	His	Ala	Gly	
Gln	Gly	Ser	Val	Ser	Ser	Ser	Thr	Thr	Thr	His	Tyr	Leu	His	Ala	Gly	
				935					940					945		
acg	acc	ttt	aag	ttt	taaaagcatg	ttatatagac	aatgcaacct	gtaaagacca	3002							
Thr	Thr	Phe	Lys	Phe												
Thr	Thr	Phe	Lys	Phe												
									950							
aatagagagt	agtgaacact	cttcaccatc	atgaatctta	tgggagaagc	taagggaat	3062										
ccacagatag	gtttccccc	taaaaattaa	gaacccgata	catctcact	agagattcga	3122										
aagaactact	taaatcctaa	gcattcga				3150										

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097850446

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Fig. 19 (con't)

gtc aca gct aaa cat att aat acg gat aat ttc tac cct gag ggt cta	1891
Val Thr Ala Lys His Ile Asn Thr Asp Asn Phe Tyr Pro Glu Gly Leu	
Val Thr Ala Lys His Ile Asn Thr Asp Asn Phe Tyr Pro Glu Gly Leu	
585	590
595	
aat aca act caa cac tac ggc tac caa ggc gtt tgg tcc cct tac tgg	1939
Asn Thr Thr Gln His Tyr Gly Tyr Gln Gly Val Trp Ser Pro Tyr Trp	
Asn Thr Thr Gln His Tyr Gly Tyr Gln Gly Val Trp Ser Pro Tyr Trp	
600	605
610	
atc gaa aca atc aca act tct gat acc tct tct gaa gat act gtg aat	1987
Ile Glu Thr Ile Thr Thr Ser Asp Thr Ser Ser Glu Asp Thr Val Asn	
Ile Glu Thr Ile Thr Thr Ser Asp Thr Ser Ser Glu Asp Thr Val Asn	
615	620
625	
act tta cat cgc cag ctt tat ggt gat tgg aca cct aca gga tat aag	2035
Thr Leu His Arg Gln Leu Tyr Gly Asp Trp Thr Pro Thr Gly Tyr Lys	
Thr Leu His Arg Gln Leu Tyr Gly Asp Trp Thr Pro Thr Gly Tyr Lys	
630	635
640	645
gta aac cca gaa aac aaa gga gac att gcc cta tct gcc ttc tgg caa	2083
Val Asn Pro Glu Asn Lys Gly Asp Ile Ala Leu Ser Ala Phe Trp Gln	
Val Asn Pro Glu Asn Lys Gly Asp Ile Ala Leu Ser Ala Phe Trp Gln	
650	655
660	
tct ttc cat aac tta ttt gcg aca cta cgt tat caa aca cag caa ggc	2131
Ser Phe His Asn Leu Phe Ala Thr Leu Arg Tyr Gln Thr Gln Gln Gly	
Ser Phe His Asn Leu Phe Ala Thr Leu Arg Tyr Gln Thr Gln Gln Gly	
665	670
675	
caa ata gca cct aca gct tct gga gaa gct act cga ctc ttc gtg cat	2179
Gln Ile Ala Pro Thr Ala Ser Gly Glu Ala Thr Arg Leu Phe Val His	
Gln Ile Ala Pro Thr Ala Ser Gly Glu Ala Thr Arg Leu Phe Val His	
680	685
690	
caa aat agc aac aat gat gcg aaa gga ttc cat atg gaa gct acg ggt	2227
Gln Asn Ser Asn Asn Asp Ala Lys Gly Phe His Met Glu Ala Thr Gly	
Gln Asn Ser Asn Asn Asp Ala Lys Gly Phe His Met Glu Ala Thr Gly	
695	700
705	
tat tct ttg gga aca acc tca aac act gct tct aat cat agc ttt ggt	2275
Tyr Ser Leu Gly Thr Thr Ser Asn Thr Ala Ser Asn His Ser Phe Gly	
Tyr Ser Leu Gly Thr Thr Ser Asn Thr Ala Ser Asn His Ser Phe Gly	
710	715
720	725
gta aac ttc tcc caa ctt ttc agt aat ctc tac gag agc cac tcc gac	2323
Val Asn Phe Ser Gln Leu Phe Ser Asn Leu Tyr Glu Ser His Ser Asp	
Val Asn Phe Ser Gln Leu Phe Ser Asn Leu Tyr Glu Ser His Ser Asp	
730	735
740	
aat tcc gtg gct tcg cat acg aca act gta gcg ctc cag aat aat aat	2371
Asn Ser Val Ala Ser His Thr Thr Thr Val Ala Leu Gln Ile Asn Asn	
Asn Ser Val Ala Ser His Thr Thr Thr Val Ala Leu Gln Ile Asn Asn	
745	750
755	
cct tgg ctg caa gag aga ttc tct aca tct gca tct cta gcc tac agc	2419
Pro Trp Leu Gln Glu Arg Phe Ser Thr Ser Ala Ser Leu Ala Tyr Ser	
Pro Trp Leu Gln Glu Arg Phe Ser Thr Ser Ala Ser Leu Ala Tyr Ser	
760	765
770	

Figure 20 (RY-44)

Restriction enzyme analysis of CPN100622

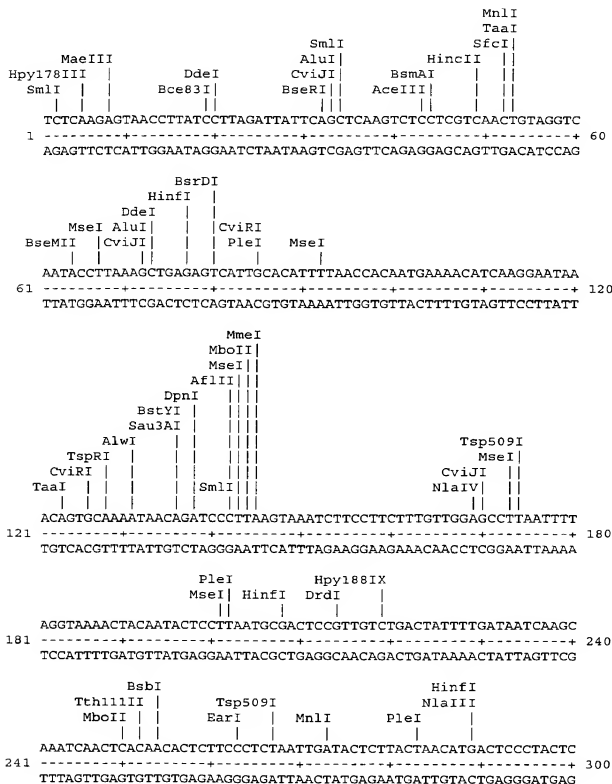




Fig. 20 (cont')

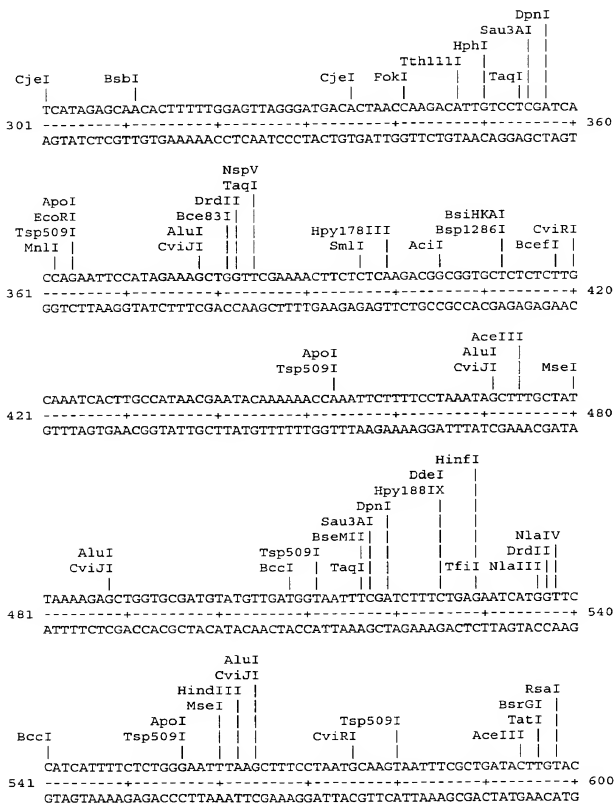
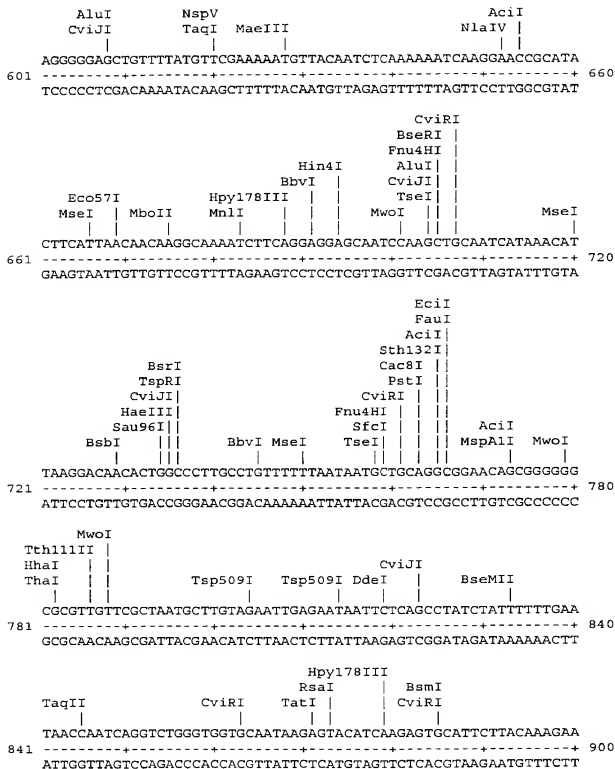


Fig. 20 (con't)



PCT/CA99/00992

[illegible]

Fig. 20 (con't)

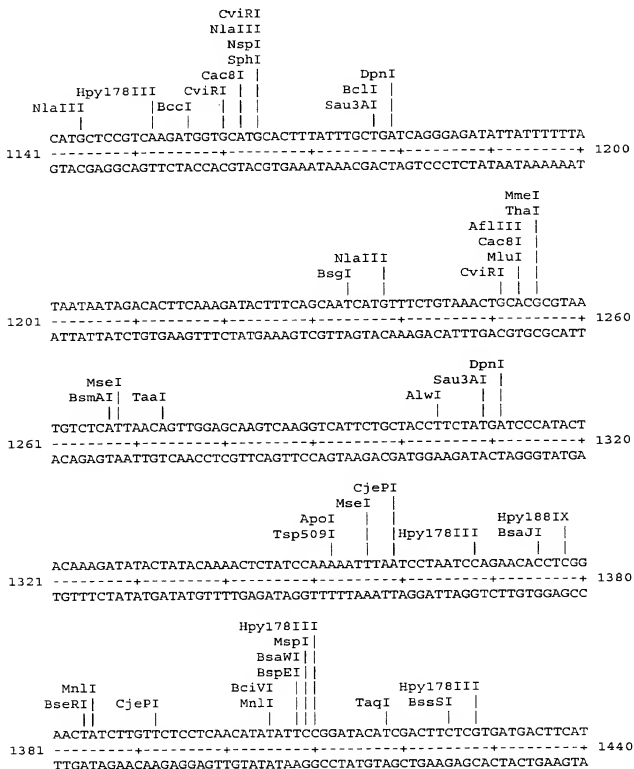


Fig. 20 (con't)

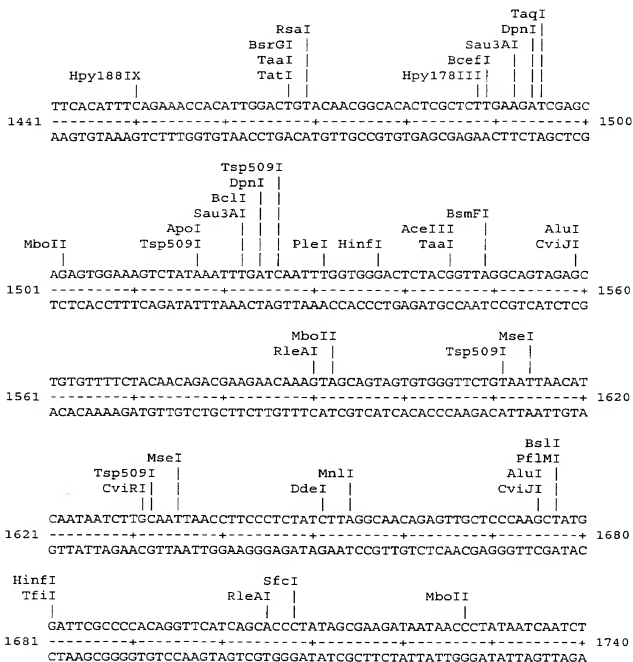


Fig. 20 (con't)

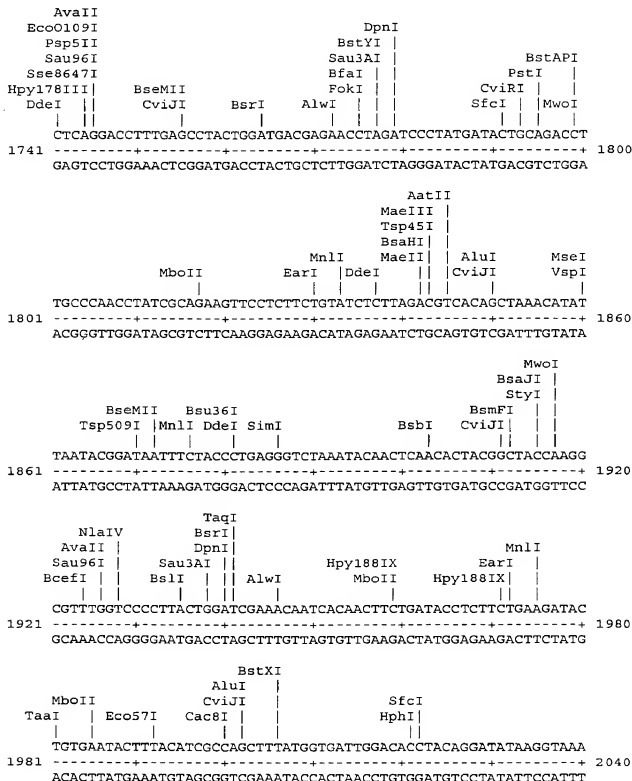


Fig. 20 (cont)

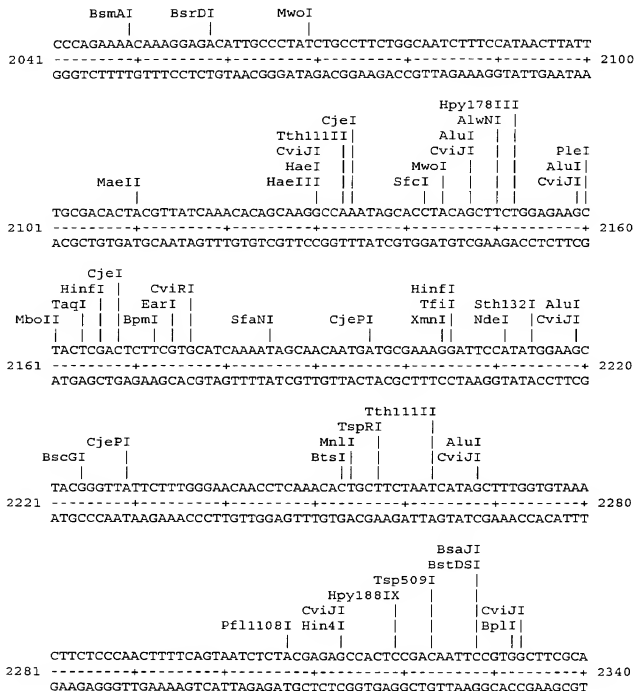


Fig. 20 (con't)

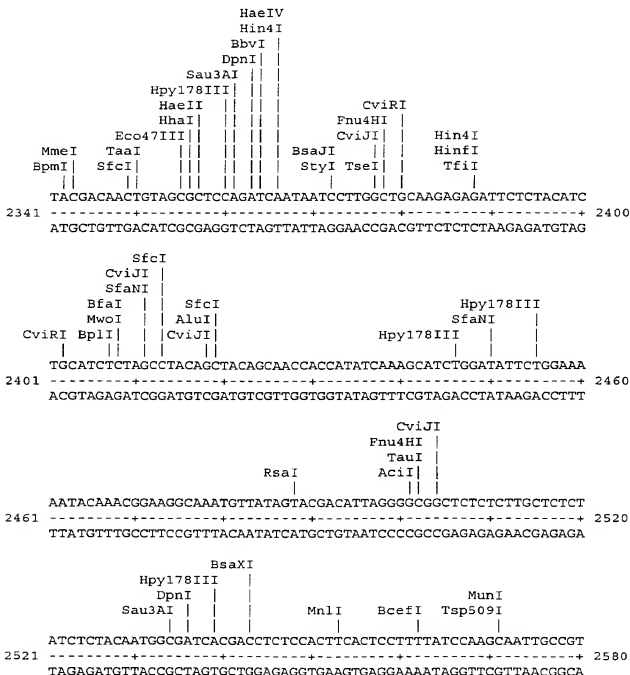




Fig. 20 (cont)

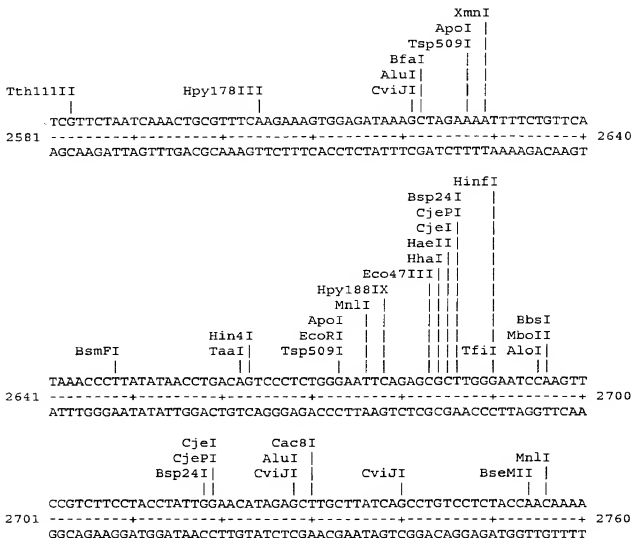


Fig. 20 (con't)

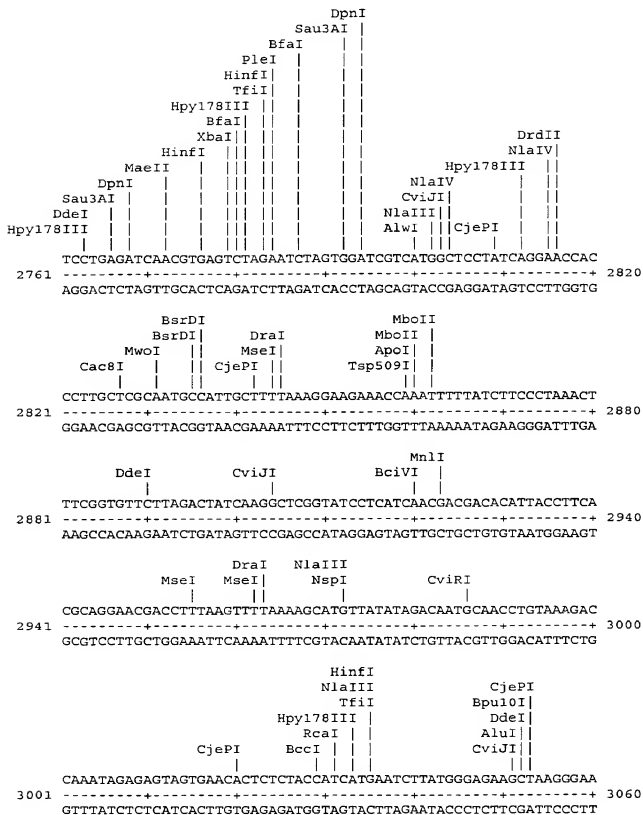


Fig. 20 (con't)

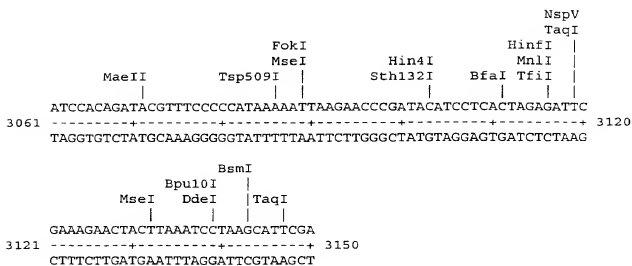


Figure 21A: CPN100626 Coding Sequence

tcttgaaactc	cactcgaaat	tactgattag	ccaaggtacg	tggacgacgc	aggccactcc	60
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cactctctcc	ttagatttag	ctgcggatatt	ttcttctctc	acgctgagtc	actactcaaa	180
ctgtggcgagt	agaatgagat	tttttacaat	aagtgaccaa	aacagaaaga	taagggaacc	240
tctagtgtca	aagactctctc	ctaagttttt	attctatctc	gggaatttca	cagcctgcac	300
tctcggggatg	actcctgcag	gttatagttt	acaaacggac	tcctctgaaa	agtttgcctt	360
agagaggatg	gaagagtttc	gtacgagctt	tcctctctta	gactctctct	ccactctaac	420
aggattttct	ccaataacta	cgtttgttgg	aaatagacat	aattcctctc	aagacattgt	480
actttctaac	tacaagtctt	ttgataacat	ccttcttctt	tggacatcgg	ctgggggagc	540
tgtgtcctgt	ataaatttct	tattatcaaa	tgttgaagac	catgctctct	tcagtaaaaa	600
tctcgcgatt	gggactggag	gcgcgattgc	ttgccaggga	gcctgacaaa	tcacgaagaa	660
tagaggacc	cttatttctt	tcagcaatgc	aggctctaac	aatgccagta	caggaggaga	720
aactcgtggg	gggtgcgattg	cctgtaatgg	agacttcacg	atttctcaaa	atccaggggc	780
tttctacttt	tccaacaatt	cgtgcaacaa	ctggggagga	gccctctcca	ccaatggaca	840
ctgcgccatc	caaaagcaaa	ggggcacctct	actctttttt	aacaatacag	ccccctagtg	900
aggggggtgcg	ctctgtagtg	aaaatacaac	gatctctgat	aacacgcgtc	ctatttattt	960
taagaaacaac	tgtgggaaca	atggcggggc	cattcaaaac	agcgttactg	ttgcgataaa	1020
aaataactcc	gggtcgggtga	ttttcaataa	caacacagcg	ttatctgttt	cgataaattc	1080
aggaatgggt	tcaggagggg	cgattttatc	aacaaacctc	tcctatgagc	ataacctgtg	1140
aactattctt	tccaataata	actactgcac	tcgcgattgc	ggagctatct	gtacacaatt	1200
tttgacaact	aaaaatagtg	gccacgtata	tttcaccaac	aatcaaggaa	actggggagc	1260
tgtctctatg	ctcctcacgg	acagcacctg	cctactcttc	gcggaaacag	gaaatatcgc	1320
atttcaaaat	aatgaggttt	tcctcacccc	atttggtaga	tacaacgcc	tacattgtac	1380
accaaatagc	aacttacaac	ttggagctaa	taagggtgat	acgactgctt	tttttgactc	1440
tatagaacac	caacatccaa	ctacaaatcc	tctaactctt	aatccccatg	cgaacacata	1500
gggaacgatc	ttatttttct	cagcctatat	cccagaagct	tttgactacg	aaaaataatt	1560
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ggcgagtat	gcaacaactg	ccaactctga	gactccatca	actagtgtag	gtctccagggt	1740
catcattaat	aaacttgcga	ttaacctccc	ctcgatctta	gcacaaaggaa	aagctcctac	1800
cttgttgatc	cgtcctctac	aatcttagtc	tcctttcaca	gaggacaata	acctcaaat	1860
tactttatca	ggctcctctga	cactcttaaa	tgaggaaaaa	cgcgactccc	acgacagtat	1920
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tcatatcaat	accgataaact	ttcatctctga	aagctttaat	gcgactgagc	attacggtta	2040
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agagacggca	aacacccctc	acagagctct	gtatgccaat	tggactcctc	taggataata	2160
ggctcaactc	gaattccaag	gagatcttgc	tacgaactcc	ctatggcaat	cctttcatac	2220
tatgttctct	ctatttaagaa	gttataatcg	aactggtgat	tctgatatcg	agagggcctt	2280
cttagaactt	caaggaatg	cgcagcgctc	ctttgttcac	caaaaataga	tcctccgggc	2340
tccaggatcc	cgtatccaat	ctacagggta	ttccttcaaa	gcactcctcg	aaactctctt	2400
acatcagaaa	atctccttag	gttttgacaa	gttcttcacc	cgcactaaag	aaatcggatc	2460
aagaacaacac	tgtctcggct	acaataacag	ctcttcaact	tatgttgtag	ttccgtgtgt	2520
ccaagaggcc	ttgtccaacat	cccacagttt	agcgtagtgc	tatggggacc	atcacctcca	2580
cgcctacatc	cgtcacatca	agaacaggcc	agaaggagac	tgtttatagc	atacatagc	2640
agcgactatc	ggctcgtctt	tcctttggca	acagaaatcc	tatcttcacc	tcagcccggt	2700
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ccgaaagtgt	gtctctcaaa	agcctttcta	taactctgac	ttacctctag	gaatccaagg	2820
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ggtactactc	caacaaaact	cccaaatcgg	tgctcacgta	cttgcgagct	gagggtctcc	2940
ggatatacta	ggcctaactc	atgtttcgaa	tgcttttagg	tacaaagctc	acaatacaac	3000
tgcgctcttc	cgtctctctg	atctattctt	ggattaccaa	ggatcggctc	cctctctcag	3060
atctacgcac	cattctccaag	cagggaagtc	cttaaaatc	taaaaataaa	gaacgataaa	3120
attgaaatct	ttagaattaa	caactatccg	atgagctacg	ttagcccaat	cggtagagga	3180
ctccttcaaa	atttcaataa					3200

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Figure 21B: CPN100626 Deduced Amino Acid Sequence

Met	Gln	Val	Phe	Pro	Lys	Val	Thr	Leu	Ser	Leu	Asp	Tyr	Ser	Ala	Asp	1	5	10	15
Ile	Ser	Ser	Ser	Thr	Leu	Ser	His	Tyr	Leu	Asn	Val	Ala	Ser	Arg	Met	20	25	30	
Arg	Phe	Leu	Thr	Ile	Ser	Asp	Gln	Asn	Arg	Lys	Ile	Lys	Glu	Pro	Leu	35	40	45	
Val	Ser	Lys	Thr	Pro	Pro	Lys	Phe	Leu	Phe	Tyr	Leu	Gly	Asn	Phe	Thr	50	55	60	
Ala	Cys	Met	Phe	Gly	Met	Thr	Pro	Ala	Val	Tyr	Ser	Leu	Gln	Thr	Asp	65	70	75	80
Ser	Leu	Glu	Lys	Phe	Ala	Leu	Glu	Arg	Asp	Glu	Glu	Phe	Arg	Thr	Ser	85	90	95	
Phe	Pro	Leu	Leu	Asp	Ser	Leu	Ser	Thr	Leu	Thr	Gly	Phe	Ser	Pro	Ile	100	105	110	
Thr	Thr	Phe	Val	Gly	Asn	Arg	His	Asn	Ser	Ser	Gln	Asp	Ile	Val	Leu	115	120	125	
Ser	Asn	Tyr	Lys	Ser	Ile	Asp	Asn	Ile	Leu	Leu	Leu	Trp	Thr	Ser	Ala	130	135	140	
Gly	Gly	Ala	Val	Ser	Cys	Asn	Asn	Phe	Leu	Leu	Ser	Asn	Val	Glu	Asp	145	150	155	160
His	Ala	Phe	Phe	Ser	Lys	Asn	Leu	Ala	Ile	Gly	Thr	Gly	Gly	Ala	Ile	165	170	175	
Ala	Cys	Gln	Gly	Ala	Cys	Thr	Ile	Thr	Lys	Asn	Arg	Gly	Pro	Leu	Ile	180	185	190	
Phe	Phe	Ser	Asn	Arg	Gly	Leu	Asn	Asn	Ala	Ser	Thr	Gly	Gly	Glu	Thr	195	200	205	
Arg	Gly	Gly	Ala	Ile	Ala	Cys	Asn	Gly	Asp	Phe	Thr	Ile	Ser	Gln	Asn	210	215	220	
Gln	Gly	Thr	Phe	Tyr	Phe	Val	Asn	Asn	Ser	Val	Asn	Asn	Trp	Gly	Gly	225	230	235	240
Ala	Leu	Ser	Thr	Asn	Gly	His	Cys	Arg	Ile	Gln	Ser	Asn	Arg	Ala	Pro	245	250	255	
Leu	Leu	Phe	Phe	Asn	Asn	Thr	Ala	Pro	Ser	Gly	Gly	Gly	Ala	Leu	Arg	260	265	270	
Ser	Glu	Asn	Thr	Thr	Ile	Ser	Asp	Asn	Thr	Arg	Pro	Ile	Tyr	Phe	Lys	275	280	285	

Fig. 21B (con't)

Asn	Asn	Cys	Gly	Asn	Asn	Gly	Gly	Ala	Ile	Gln	Thr	Ser	Val	Thr	Val	290	295	300	
Ala	Ile	Lys	Asn	Asn	Ser	Gly	Ser	Val	Ile	Phe	Asn	Asn	Asn	Thr	Ala	305	310	315	320
Leu	Ser	Gly	Ser	Ile	Asn	Ser	Gly	Asn	Gly	Ser	Gly	Gly	Ala	Ile	Tyr	325	330	335	
Thr	Thr	Asn	Leu	Ser	Ile	Asp	Asp	Asn	Pro	Gly	Thr	Ile	Leu	Phe	Asn	340	345	350	
Asn	Asn	Tyr	Cys	Ile	Arg	Asp	Gly	Gly	Ala	Ile	Cys	Thr	Gln	Phe	Leu	355	360	365	
Thr	Ile	Lys	Asn	Ser	Gly	His	Val	Tyr	Phe	Thr	Asn	Asn	Gln	Gly	Asn	370	375	380	
Trp	Gly	Gly	Ala	Leu	Met	Leu	Leu	Gln	Asp	Ser	Thr	Cys	Leu	Leu	Phe	385	390	395	400
Ala	Glu	Gln	Gly	Asn	Ile	Ala	Phe	Gln	Asn	Asn	Glu	Val	Phe	Leu	Thr	405	410	415	
Thr	Phe	Gly	Arg	Tyr	Asn	Ala	Ile	His	Cys	Thr	Pro	Asn	Ser	Asn	Leu	420	425	430	
Gln	Leu	Gly	Ala	Asn	Lys	Gly	Tyr	Thr	Thr	Ala	Phe	Phe	Asp	Pro	Ile	435	440	445	
Glu	His	Gln	His	Pro	Thr	Thr	Asn	Pro	Leu	Ile	Phe	Asn	Pro	Asn	Ala	450	455	460	
Asn	His	Gln	Gly	Thr	Ile	Leu	Phe	Ser	Ser	Ala	Tyr	Ile	Pro	Glu	Ala	465	470	475	480
Ser	Asp	Tyr	Glu	Asn	Asn	Phe	Ile	Ser	Ser	Ser	Lys	Asn	Thr	Ser	Glu	485	490	495	
Leu	Arg	Asn	Gly	Val	Leu	Ser	Ile	Glu	Asp	Arg	Ala	Gly	Trp	Gln	Phe	500	505	510	
Tyr	Lys	Phe	Thr	Gln	Lys	Gly	Gly	Ile	Leu	Lys	Leu	Gly	His	Ala	Ala	515	520	525	
Ser	Ile	Ala	Thr	Thr	Ala	Asn	Ser	Glu	Thr	Pro	Ser	Thr	Ser	Val	Gly	530	535	540	
Ser	Gln	Val	Ile	Ile	Asn	Asn	Leu	Ala	Ile	Asn	Leu	Pro	Ser	Ile	Leu	545	550	555	560
Ala	Lys	Gly	Lys	Ala	Pro	Thr	Leu	Trp	Ile	Arg	Pro	Leu	Gln	Ser	Ser	565	570	575	

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Fig. 21B (con't)

Ala	Pro	Phe	Thr	Glu	Asp	Asn	Asn	Pro	Thr	Ile	Thr	Leu	Ser	Gly	Pro	580	585	590
Leu	Thr	Leu	Leu	Asn	Glu	Glu	Asn	Arg	Asp	Pro	Tyr	Asp	Ser	Ile	Asp	595	600	605
Leu	Ser	Glu	Pro	Leu	Gln	Asn	Ile	His	Leu	Leu	Ser	Leu	Ser	Asp	Val	610	615	620
Thr	Ala	Arg	His	Ile	Asn	Thr	Asp	Asn	Phe	His	Pro	Glu	Ser	Leu	Asn	625	630	635
Ala	Thr	Glu	His	Tyr	Gly	Tyr	Gln	Gly	Ile	Trp	Ser	Pro	Tyr	Trp	Val	645	650	655
Glu	Thr	Ile	Thr	Thr	Asn	Asn	Ala	Ser	Ile	Glu	Thr	Ala	Asn	Thr		660	665	670
Leu	Tyr	Arg	Ala	Leu	Tyr	Ala	Asn	Trp	Thr	Pro	Leu	Gly	Tyr	Lys	Val	675	680	685
Asn	Pro	Glu	Tyr	Gln	Gly	Asp	Leu	Ala	Thr	Thr	Pro	Leu	Trp	Gln	Ser	690	695	700
Phe	His	Thr	Met	Phe	Ser	Leu	Leu	Arg	Ser	Tyr	Asn	Arg	Thr	Gly	Asp	705	710	715
Ser	Asp	Ile	Glu	Arg	Pro	Phe	Leu	Glu	Ile	Gln	Gly	Ile	Ala	Asp	Gly	725	730	735
Leu	Phe	Val	His	Gln	Asn	Ser	Ile	Pro	Gly	Ala	Pro	Gly	Phe	Arg	Ile	740	745	750
Gln	Ser	Thr	Gly	Tyr	Ser	Leu	Gln	Ala	Ser	Ser	Glu	Thr	Ser	Leu	His	755	760	765
Gln	Lys	Ile	Ser	Leu	Gly	Phe	Ala	Gln	Phe	Phe	Thr	Arg	Thr	Lys	Glu	770	775	780
Ile	Gly	Ser	Ser	Asn	Asn	Val	Ser	Ala	His	Asn	Thr	Val	Ser	Ser	Leu	785	790	795
Tyr	Val	Glu	Leu	Pro	Trp	Phe	Gln	Glu	Ala	Phe	Ala	Thr	Ser	His	Ser	805	810	815
Leu	Ala	Tyr	Gly	Tyr	Gly	Asp	His	His	Leu	His	Ala	Tyr	Ile	Arg	His	820	825	830
Ile	Lys	Asn	Arg	Ala	Glu	Gly	Thr	Cys	Tyr	Ser	His	Thr	Leu	Ala	Ala	835	840	845
Ala	Ile	Gly	Cys	Ser	Phe	Pro	Trp	Gln	Gln	Lys	Ser	Tyr	Leu	His	Leu	850	855	860

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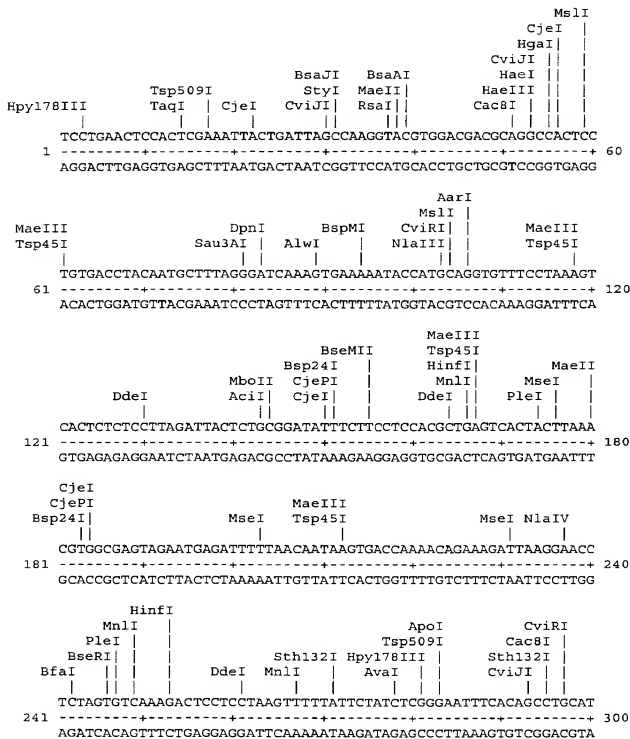
Fig. 21B (con't)

Ser	Pro	Phe	Val	Gln	Ala	Ile	Ala	Ile	Arg	Ser	His	Gln	Thr	Ala	Phe	865	870	875	880
Glu	Glu	Ile	Gly	Asp	Asn	Pro	Arg	Lys	Phe	Val	Ser	Gln	Lys	Pro	Phe	885	890	895	
Tyr	Asn	Leu	Thr	Leu	Pro	Leu	Gly	Ile	Gln	Gly	Lys	Trp	Gln	Ser	Lys	900	905	910	
Phe	His	Val	Pro	Thr	Glu	Trp	Thr	Leu	Glu	Leu	Ser	Tyr	Gln	Pro	Val	915	920	925	
Leu	Tyr	Gln	Gln	Asn	Pro	Gln	Ile	Gly	Val	Thr	Leu	Leu	Ala	Ser	Gly	930	935	940	
Gly	Ser	Trp	Asp	Ile	Leu	Gly	His	Asn	Tyr	Val	Arg	Asn	Ala	Leu	Gly	945	950	955	960
Tyr	Lys	Val	His	Asn	Gln	Thr	Ala	Leu	Phe	Arg	Ser	Leu	Asp	Leu	Phe	965	970	975	
Leu	Asp	Tyr	Gln	Gly	Ser	Val	Ser	Ser	Thr	Ser	Thr	His	His	Leu		980	985	990	
Gln	Ala	Gly	Ser	Thr	Leu	Lys	Phe									995	1000		



Figure 22 (RY-45)

Restriction enzyme analysis of CPN100626



Hpy178III  
 BtsI  
 FokI  
 PstI  
 NlaIII  
 CviRI  
 SfcI  
 TspRI  
 PleI  
 HinFI  
 MnlI  
 NspI  
 HinFI  
 GTTCGGGATGACTCCTGCAGTGTATAGTTTACAAACGGACTCCCTTGAAAGGTTTGCTTT  
 301  
 CAAGCCCTACTGAGGACGTACATATCAAATGTTTGCCTGAGGGAACCTTTCAAACGAAA  
 360  
 Hin4I  
 AluI  
 CviJI  
 MboII  
 RsaI  
 FokI  
 SunI  
 EarI  
 XmnI  
 BpI  
 BsaXI  
 Hin4I  
 MnlI  
 HinfI  
 DdeI  
 PleI  
 AGAGAGGGATGAAGAGTTTCGTACGAGCTTTCTCTCTTAGACTCTCTCTCCACTCTTAC  
 361  
 TCTCTCCCTACTTCTCAAAGCATGCTCGAAAGGAGAGAATCTGAGAGAGAGGTGAGAATG  
 420  
 CjeI  
 MaeII  
 Bce83I  
 Tsp509I  
 Hpy178III  
 SmlI  
 RsaI  
 TatI  
 MmeI  
 AGGATTTTCTCCAATAACTACGTTTGTGGAAATAGACATAATTCTCTCAAGACATTGT  
 421  
 TCCTAAAAGAGGTTATTGTATGCAAAACAACCTTTATCTGTATTAAGGAGAGTTCTGTAAACA  
 480  
 Bsp24I  
 CjeI  
 CjePI  
 AceIII  
 CviJI  
 MwoI  
 AluI  
 CviJI  
 FokI  
 MboII  
 ACTTTCTAACTACAAGTCTATTGATAACATCCTTCTTCTTTGGACATCGGGCTGGGGGAGC  
 481  
 TGAAAGATTGATGTTTCAGATAACTATTGTAGGAAGAAGAACTCTGAGCCGACCCCTCG  
 540  
 Tsp509I  
 CjeI  
 CjePI  
 Bsp24I  
 MboII  
 NlaIII  
 BbsI  
 Eco57I  
 MboII  
 CjePI  
 TGIGTCTCTGAATAATTTCTTATTATCAAATGTTGAAGACCATGCCTTCTTCAGTAAAAA  
 541  
 ACACAGGCATTATTAAAGAATAATAGTTTACAACCTCTCGTACGGAAGAAGTCATTTTT  
 600

Hpy178III  
 CviRI  
 Cac8I  
 CviJI  
 NlaIV  
 BpmI  
 ScrFI  
 BsaJI  
 EcoRII  
 Cac8I  
 CjePI  
 BsgI  
 BsrI BsmFI  
 Tth111II HhaI  
 NruI  
 ThaI  
 MnlI  
 TCTCGCGATTGGGACTGGAGGCGGATTGCTTCGCAGGGAGCCTGCACAATCACGAAGAA  
 601  
 AGAGCGCTAACCTTGACCTCCGCGCTAACGAACGGTCCCTCGSACGTGTAGTGCTTCTT  
 MboII  
 NlaIV  
 AvaII  
 EcoO109I  
 Psp5II  
 Sau96I  
 SimI  
 MnlI  
 TaqI  
 MseI  
 RsaI  
 MnlI  
 TatI  
 TAGAGGACCCCTTATTTTTTTCAGCAATCGAGGTCTTAACAATCGAGTACAGGAGGAGA  
 661  
 ATCTCCTGGGGAATAAAAAAGTCGTAGCTCCAGAAATGTTACGCTCATGTCTCCTCTT  
 BssSI BseRI  
 BsmAI  
 Hpy178III  
 AACTCGTGGGGGTGCGATTGCCTGAATGGAGACTTCACGATTCTCAAATCAAGGGAC  
 721  
 TTGAGCACCCCCACGCTAACCGACATTACCTCTGAAGTGCTAAAGAGTTTATGTTCCCTGT  
 BanII  
 Bsp1286I  
 BsrI  
 Tsp509I  
 HincII  
 BsmFI  
 HincII  
 BmrI  
 MnlI  
 CviJI  
 Hin4I  
 NlaIV  
 FokI  
 MnlI  
 BseRI  
 BplI  
 TTTCTACTTTGTCAACAATTCCTGCAACAACTGGGGAGGAGCCCTCTCCACCAATGGACA  
 781  
 AAAGATGAAACAGTTGTTAAGGCAGTTGTTGACCCCTCCTCGGAGAGGTGGTGTACCTGT  
 840

Fig. 22 (con't)

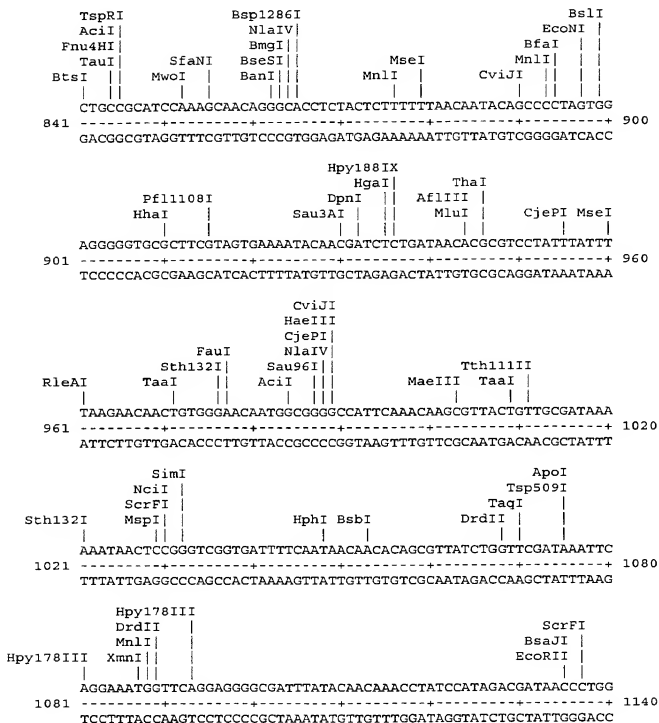


Fig. 22 (con't)

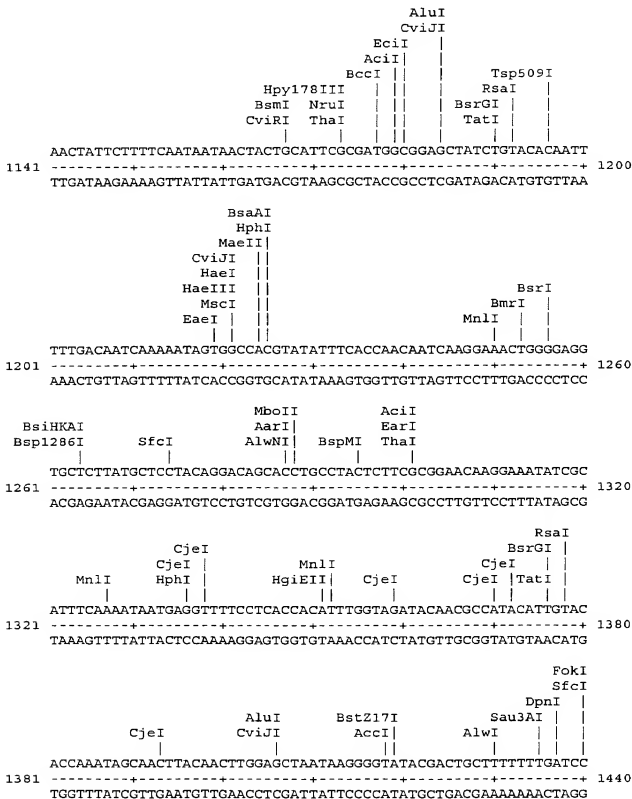


Fig. 22 (cont')

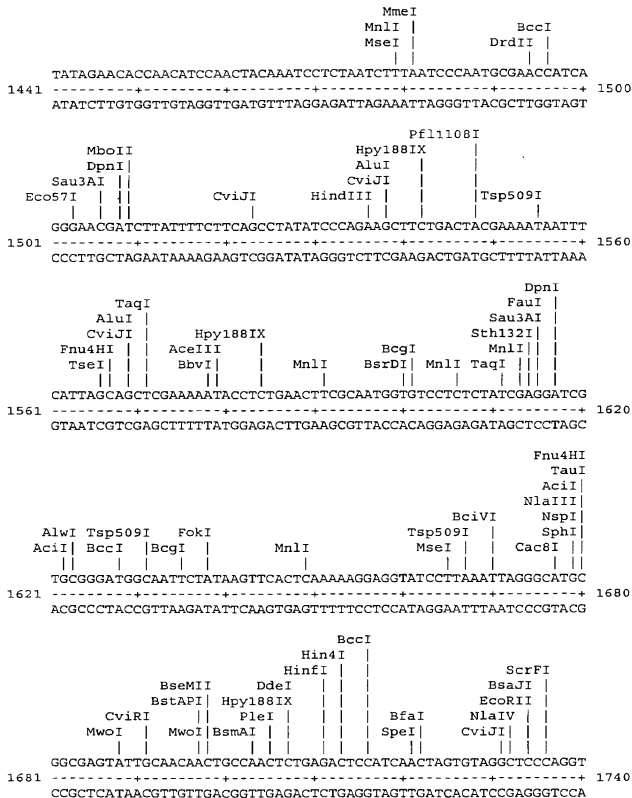


Fig. 22 (cont)

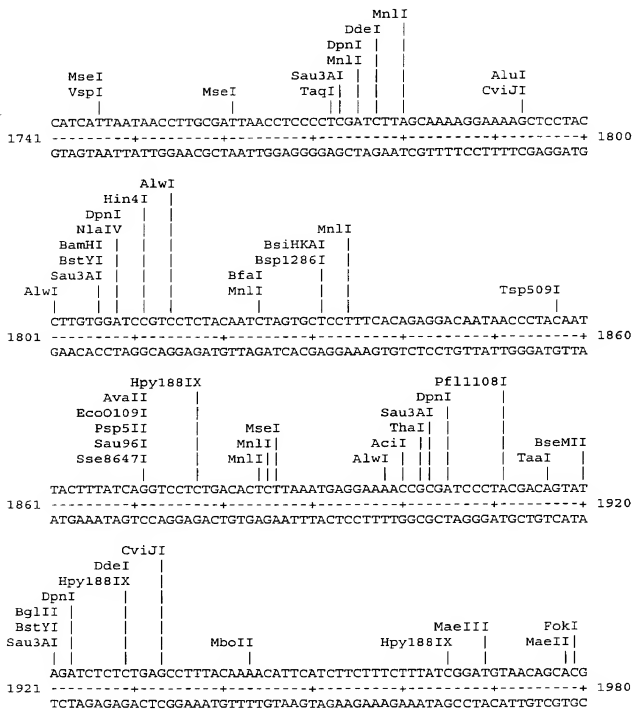
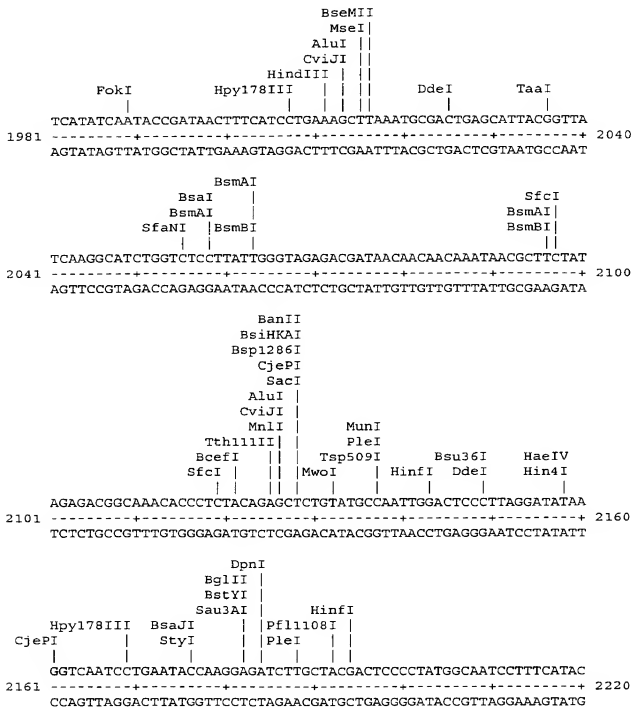


Fig. 22 (con't)





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CviJI  
 HaeI  
 HaeIII  
 Hpy178III  
 TaqI  
 HphI  
 EcoRV  
 MnlI  
 Hpy188IX  
 HinfI  
 TfiI  
 BsrI  
 MseI  
 TaqI  
 StuI  
 2221  
 TATGTTCTCTCTATTAAGAAGTTATAATCGAACTGGTGATTCTGATATCGAGAGGCCCTTT  
 ATACAAGAGAGATAATTCTTCAATATTAGCTTGACCACTAAGACTATAGCTCTCCGGAAA  
 2280  
 NlaIV  
 Sth132I  
 CviJI  
 SfaNI  
 NciI  
 ScrFI  
 SmaI  
 BsaJI  
 MspI  
 NciI  
 ScrFI  
 ApoI  
 Tsp509I  
 DdeI  
 CviJI  
 HaeIII  
 BceFI  
 MnlI  
 FokI  
 Sth132I  
 BpmI  
 BsaJI  
 AvaiI  
 2281  
 CTTAGAAATTC AAGGATTGCCGACGGCCTCTTGTTCATCAAATAGCATCCCCGGGGC  
 GAATCTTTAAGTTCCCTAACGGCTGCCGGAGAAACAAGTAGTTTTATCGTAGGGGCCCG  
 2340  
 HaeIV  
 HinfI  
 TfiI  
 ScrFI  
 BanII  
 Bsp1286I  
 EcoRII  
 BciVI  
 SfcI  
 FokI  
 MnlI  
 Tth111III  
 SfaNI  
 Hpy188IX  
 2341  
 TCCAGGATTCGATCCAATCTACAGGGTATTCCTTACAAGCATCCTCCGAAACTTCTTT  
 AGGTCCTAAGGCATAGGTTAGATGTCCCATAAGGAATGTTCTGATAGGAGGCTTTTGAAGAAA  
 2400

Fig. 22 (cont')

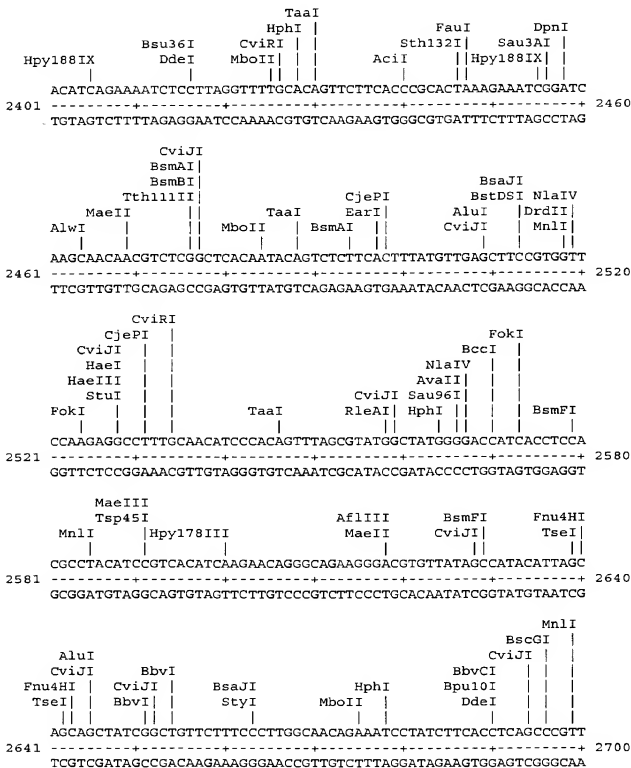


Fig. 22 (cont')

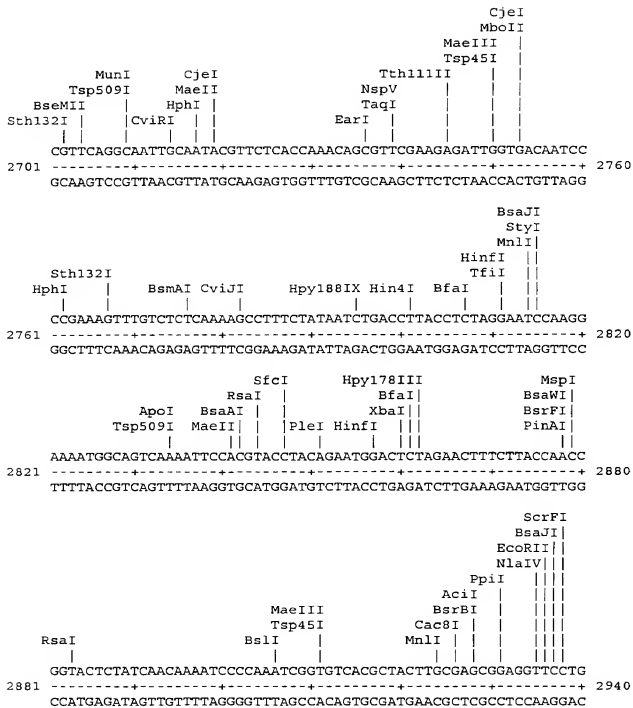


Fig. 22 (cont)

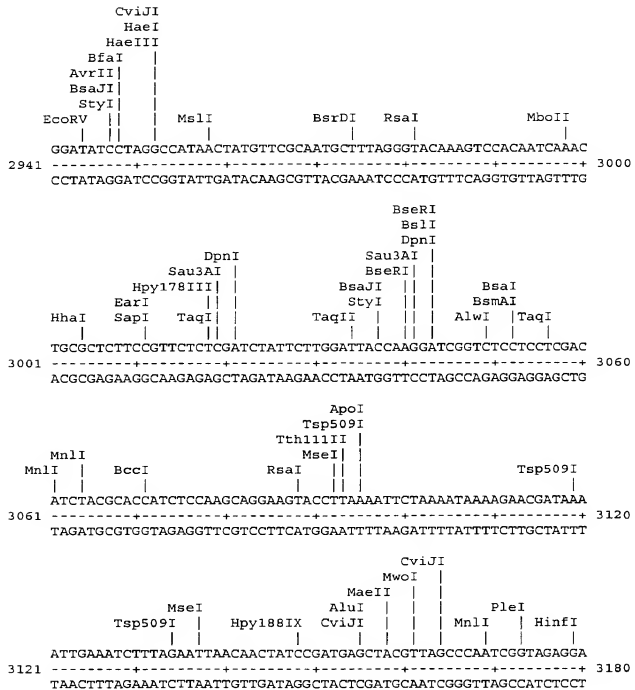


Fig. 22 (con't)

```

                                DraI
                                MnlI
                                SmaI
                                MseI|
                                |
                                ApoI  ||
                                Tsp509I ||
                                |      ||
CTCCCTCAAAATTTAAATAA
3181 -----+----- 3200
GAGGGAGTTTTAAATTTATT
```

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PCT/CA99/00992

Figure 23:

```

tagacactat aaaacaaatt atagacaaaa aatctagcat tgatttatcc agaatatctc 60

ttctctatttg tgaacgagta tgcgcttttt ttgcttcgga atg ttg ctt cct ttt 115
Met Leu Leu Pro Phe
1 5

act ttt gta ttg gct aat gaa ggt ctc caa ctt cct ttg gag acc tat 163
Thr Phe Val Leu Ala Asn Glu Gly Leu Gln Leu Pro Leu Glu Thr Tyr
10 15 20

att aca tta agt cct gaa tat caa gca gcc cct caa gta ggg ttt act 211
Ile Thr Leu Ser Pro Glu Tyr Gln Ala Ala Pro Gln Val Gly Phe Thr
25 30 35

cat aac caa aat caa gat ctc gca att gtc ggg aat cac aat gat ttc 259
His Asn Gln Asn Gln Asp Leu Ala Ile Val Gly Asn His Asn Asp Phe
40 45 50

atc ttg gac tat aag tac tat cgg tcg aat gga ggt gct ctt acc tgt 307
Ile Leu Asp Tyr Lys Tyr Tyr Arg Ser Asn Gly Gly Ala Leu Thr Cys
55 60 65

aag aat ctt ctg atc tct gaa aat ata ggg aat gtc ttc ttt gag aag 355
Lys Asn Leu Leu Ile Ser Glu Asn Ile Gly Asn Val Phe Phe Glu Lys
70 75 80 85

aat gtc tgt ccc aat tct ggc ggg gca att tat gct gct caa aat tgc 403
Asn Val Cys Pro Asn Ser Gly Gly Ala Ile Tyr Ala Ala Gln Asn Cys
90 95 100

acg atc tcc aag aat cag aac tat gca ttt act aca aac ttg gtc tct 451
Thr Ile Ser Lys Asn Gln Asn Tyr Ala Phe Thr Thr Asn Leu Val Ser
105 110 115

gac aat cct aca gcc act gcg gga tca cta ttg ggt gga gct ctc ttt 499
Asp Asn Pro Thr Ala Thr Ala Gly Ser Leu Leu Gly Gly Ala Leu Phe
120 125 130

gcc ata aat tgc tct att act aat aac cta gga cag gga act ttc gtt 547
Ala Ile Asn Cys Ser Ile Thr Asn Asn Leu Gly Gln Gly Thr Phe Val
135 140 145

gac aat ctc gct tta aat aag ggg ggt gcc ctc tat act gag acg aac 595
Asp Asn Leu Ala Leu Asn Lys Gly Gly Ala Leu Tyr Thr Glu Thr Asn
150 155 160 165

tta tct att aaa gac aat aaa ggc ccg atc ata atc aag cag aat cgg 643
Leu Ser Ile Lys Asp Asn Lys Gly Pro Ile Ile Ile Lys Gln Asn Arg
170 175 180

gca cta aat tcg gac agt tta gga gga ggg att tat agt ggg aac tct 691
Ala Leu Asn Ser Asp Ser Leu Gly Gly Gly Ile Tyr Ser Gly Asn Ser
185 190 195

```

Title: CHLAMYDIA ANTIGENS AND  
CORRESPONDING DNA FRAGMENTS  
AND USES THEREOF

Inventor(s): Andrew D. MURDIN et al  
DOCKET NO.: 032931/0251

097830446

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Fig. 23 (cont')

cta aat ata gag gga aat tct gga gct ata cag atc aca agc aac tct Leu Asn Ile Glu Gly Asn Ser Gly Ala Ile Gln Ile Thr Ser Asn Ser 200 205 210	739
tca gga tct ggg gga ggc ata ttt tct acc caa aca ctc acg atc tcc Ser Gly Ser Gly Gly Ile Phe Ser Thr Gln Thr Leu Thr Ile Ser 215 220 225	787
tcg aat aaa aaa ctc ata gaa atc agt gaa aat tcc gcg ttc gca aat Ser Asn Lys Lys Leu Ile Glu Ile Ser Glu Asn Ser Ala Phe Ala Asn 230 235 240 245	835
aac tat gga tcg aac ttc aat cca gga gga gga ggt ctt act acc acc Asn Tyr Gly Ser Asn Phe Asn Pro Gly Gly Gly Leu Thr Thr Thr 250 255 260	883
ttt tgc acg ata ttg aac aac cga gaa ggg gta ctc ttt aac aat aac Phe Cys Thr Ile Leu Asn Asn Arg Glu Gly Val Leu Phe Asn Asn Asn 265 270 275	931
caa agc cag agc aac ggt gga gcc att cat gcg aaa tct atc att atc Gln Ser Gln Ser Asn Gly Gly Ala Ile His Ala Lys Ser Ile Ile Ile 280 285 290	979
aaa gaa aat ggt cct gta tac ttt tta aat aac act gca act cgg gga Lys Glu Asn Gly Pro Val Tyr Phe Leu Asn Asn Thr Ala Thr Arg Gly 295 300 305	1027
ggg gct ctc ctc aac tta tca gca ggt tct gga aac gga agc ttc atc Gly Ala Leu Leu Asn Leu Ser Ala Gly Ser Gly Asn Gly Ser Phe Ile 310 315 320 325	1075
tta tct gca gat aat gga gat att atc ttt aac aat aat acg gcc tcc Leu Ser Ala Asp Asn Gly Asp Ile Ile Phe Asn Asn Asn Thr Ala Ser 330 335 340	1123
aag cat gcc ctc aat cct cca tac aga aac gcc att cac tcg act cct Lys His Ala Leu Asn Pro Pro Tyr Arg Asn Ala Ile His Ser Thr Pro 345 350 355	1171
aat atg aat ctg caa ata gga gcc cgt ccc gcc tat cga gtg ctg ttc Asn Met Asn Leu Gln Ile Gly Ala Arg Pro Gly Tyr Arg Val Leu Phe 360 365 370	1219
tat gat ccc ata gaa cat gag ctc cct tcc tcc ttc ccc ata ctc ttt Tyr Asp Pro Ile Glu His Glu Leu Pro Ser Ser Phe Pro Ile Leu Phe 375 380 385	1267
aat ttc gaa acc ggt cat aca ggt aca gtt tta ttt tca ggg gaa cat Asn Phe Glu Thr Gly His Thr Gly Thr Val Leu Phe Ser Gly Glu His 390 395 400 405	1315

Fig. 23 (con't)

gta cac cag aac ttt acc gat gaa atg aat ttc ttt tcc tat tta agg	1363
Val His Gln Asn Phe Thr Asp Glu Met Asn Phe Phe Ser Tyr Leu Arg	
410 415	
aac act tcg gaa cta cgt caa gga gtc ctt gct gtt gaa gat ggt gcg	1411
Asn Thr Ser Glu Leu Arg Gln Gly Val Leu Ala Val Glu Asp Gly Ala	
425 430 435	
ggg ctg gcc tgc tat aag ttc ttc caa cga gga ggc act cta ctt cta	1459
Gly Leu Ala Cys Tyr Lys Phe Phe Gln Arg Gly Gly Thr Leu Leu Leu	
440 445 450	
ggg caa ggt gcg gtg atc acg aca gca gga acg att ccc aca cca tcc	1507
Gly Gln Gly Ala Val Ile Thr Thr Ala Gly Thr Ile Pro Thr Pro Ser	
455 460 465	
tca aca cca acg aca gta gga agt act ata act tta aat cac att gcc	1555
Ser Thr Pro Thr Thr Val Gly Ser Thr Ile Thr Leu Asn His Ile Ala	
470 475 480 485	
att gac ctt cct tct att ctt tct ttt caa gct cag gct cca aaa att	1603
Ile Asp Leu Pro Ser Ile Leu Ser Phe Gln Ala Gln Ala Pro Lys Ile	
490 495 500	
tgg att tac ccc aca aaa aca gga tct acc tat act gaa gat tcc aac	1651
Trp Ile Tyr Pro Thr Lys Thr Gly Ser Thr Tyr Thr Glu Asp Ser Asn	
505 510 515	
ccg aca atc aca atc tca gga act ctc acc tta cgc aac agc aac aac	1699
Pro Thr Ile Thr Ile Ser Gly Thr Leu Thr Leu Arg Asn Ser Asn Asn	
520 525 530	
gaa gat ccc tac gat agt ctg gat ctc tcg cac tct ctt gag aaa gtt	1747
Glu Asp Pro Tyr Asp Ser Leu Asp Leu Ser His Ser Leu Glu Lys Val	
535 540 545	
ccc ctt ctt tat att gtc gat gtc gct gca caa aaa att aac tct tcg	1795
Pro Leu Leu Tyr Ile Val Asp Val Ala Ala Gln Lys Ile Asn Ser Ser	
550 555 560 565	
caa ctg gat cta tcc aca tta aat tct ggc gaa cac tat ggg tat caa	1843
Gln Leu Asp Leu Ser Thr Leu Asn Ser Gly Glu His Tyr Gly Tyr Gln	
570 575 580	
ggc atc tgg tcg acc tat tgg gta gaa act aca aca atc acg aac cct	1891
Gly Ile Trp Ser Thr Tyr Trp Val Glu Thr Thr Thr Ile Thr Asn Pro	
585 590 595	
aca tct cta cta ggc gcg aat aca aaa cac aag ctg ctc tat gca aac	1939
Thr Ser Leu Leu Gly Ala Asn Thr Lys His Lys Leu Leu Tyr Ala Asn	
600 605 610	



Fig. 23 (con't)

tgg	tct	cct	cta	ggc	tac	cgt	cct	cat	ccc	gaa	cgt	cga	gga	gaa	ttc	1987
Trp	Ser	Pro	Leu	Gly	Tyr	Arg	Pro	His	Pro	Glu	Arg	Arg	Gly	Glu	Phe	
615						620					625					
att	acg	aat	gcc	ttg	tgg	caa	tcg	gca	tat	acg	gct	ctt	gca	gga	ctc	2035
Ile	Thr	Asn	Ala	Leu	Trp	Gln	Ser	Ala	Tyr	Thr	Ala	Leu	Ala	Gly	Leu	
630						635				640					645	
cac	tcc	ctc	tcc	tcc	tgg	gat	gaa	gag	aag	ggt	cat	gca	gct	tcc	cta	2083
His	Ser	Leu	Ser	Ser	Trp	Asp	Glu	Gly	Lys	Gly	His	Ala	Ala	Ser	Leu	
				650					655					660		
caa	ggc	att	ggt	ctt	ctg	ggt	cat	caa	aaa	gac	aaa	aac	ggt	ttt	aag	2131
Gln	Gly	Ile	Gly	Leu	Leu	Val	His	Gln	Lys	Asp	Lys	Asn	Gly	Phe	Lys	
			665				670						675			
gga	ttt	cgt	agt	cat	atg	aca	ggt	tat	agt	gct	acc	acc	gaa	gca	acc	2179
Gly	Phe	Arg	Ser	His	Met	Thr	Gly	Tyr	Ser	Ala	Thr	Thr	Glu	Ala	Thr	
		680					685					690				
tct	tct	caa	agt	ccg	aat	ttc	tct	tta	gga	ttt	gct	cag	ttc	ttc	tcc	2227
Ser	Ser	Gln	Ser	Pro	Asn	Phe	Ser	Leu	Gly	Phe	Ala	Gln	Phe	Phe	Ser	
		695				700					705					
aaa	gct	aaa	gaa	cat	gaa	tct	caa	aat	agc	acg	tcc	tct	cac	cac	tat	2275
Lys	Ala	Lys	Glu	His	Glu	Ser	Gln	Asn	Ser	Thr	Ser	Ser	His	His	Tyr	
710					715					720					725	
ttc	tct	gga	atg	tgc	ata	gca	aaa	tac	tct	ctt	caa	aga	gtg	ata	cgt	2323
Phe	Ser	Gly	Met	Cys	Ile	Ala	Lys	Tyr	Ser	Leu	Gln	Arg	Val	Ile	Arg	
			730					735					740			
cta	tct	gtg	tct	ctt	gct	tat	atg	ttt	acc	tcg	gaa	cat	acc	cat	aca	2371
Leu	Ser	Val	Ser	Leu	Ala	Tyr	Met	Phe	Thr	Ser	Glu	His	Thr	His	Thr	
			745					750					755			
atg	tat	cag	ggt	ctc	ctg	gaa	ggg	aac	tct	cag	gga	tct	ttc	cac	aac	2419
Met	Tyr	Gln	Gly	Leu	Leu	Gly	Asn	Ser	Gln	Gly	Ser	Phe	His	Asn		
		760					765					770				
cat	acc	tta	gca	ggg	gct	ctc	tcc	tgt	ggt	ttc	tta	cct	caa	cct	cac	2467
His	Thr	Leu	Ala	Gly	Ala	Leu	Ser	Cys	Val	Phe	Leu	Pro	Gln	Pro	His	
		775				780					785					
ggc	gag	tcc	ctg	cag	atc	tat	ccc	ttt	att	act	gcc	tta	gcc	atc	cga	2515
Gly	Glu	Ser	Leu	Gln	Ile	Tyr	Pro	Phe	Ile	Thr	Ala	Leu	Ala	Ile	Arg	
790					795					800					805	
gga	aat	ctt	gct	gcg	ttt	caa	gaa	tct	gga	gac	cat	gct	cgg	gaa	ttt	2563
Gly	Asn	Leu	Ala	Ala	Phe	Gln	Glu	Ser	Gly	Asp	His	Ala	Arg	Glu	Phe	
				810					815					820		

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Fig. 23 (con't)

tcc cta cac cgc ccc cta acg gac gtc tcc ctc cct gta gga atc cgc	2611
Ser Leu His Arg Pro Leu Thr Asp Val Ser Leu Pro Val Gly Ile Arg	
825 830 835	
gct tct tgg aag aac cac cac cga gtt ccc cta gtc tgg ctc aca gaa	2659
Ala Ser Trp Lys Asn His His Arg Val Pro Leu Val Trp Leu Thr Glu	
840 845 850	
att tcc tat cgc tct act ctc tat agg caa gat cct gaa ctc cac tcg	2707
Ile Ser Tyr Arg Ser Thr Leu Tyr Arg Gln Asp Pro Glu Leu His Ser	
855 860 865	
aaa tta ctg att agc caa ggt acg tgg acg acg cag gcc act cct gtg	2755
Lys Leu Leu Ile Ser Gln Gly Thr Trp Thr Thr Gln Ala Thr Pro Val	
870 875 880 885	
acc tac aat gct tta ggg atc aaa gtg aaa aat acc atg cag gtg ttt	2803
Thr Tyr Asn Ala Leu Gly Ile Lys Val Lys Asn Thr Met Gln Val Phe	
890 895 900	
cct aaa gtc act ctc tcc tta gat tac tct gcg gat att tct tcc tcc	2851
Pro Lys Val Thr Leu Ser Leu Asp Tyr Ser Ala Asp Ile Ser Ser Ser	
905 910 915	
acg ctg agt cac tac tta aac gtg gcg agt aga atg aga ttt	2893
Thr Leu Ser His Tyr Leu Asn Val Ala Ser Arg Met Arg Phe	
920 925 930	
taacaataag tgaccaaacc agaaagatta aggaacctct agtgtcaaag actcctccta	2953
agttttttatt ctatctcggg aatttcacag cctgcattgt cgggatg	3000

Figure 24 (RY-46)

Restriction enzyme analysis of CPN100628



Inventor(s): Andrew D. MURDIN et al  
DOCKET NO.: 032931/0251

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Fig. 24 (con't)

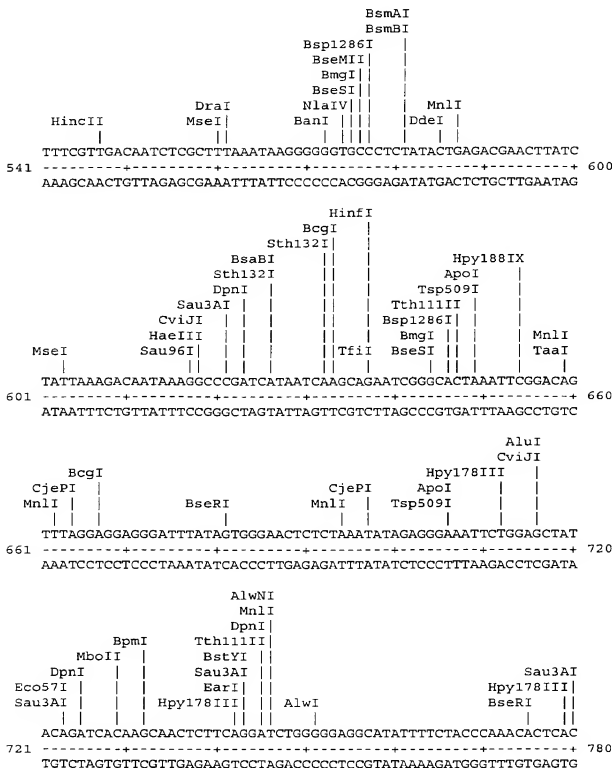
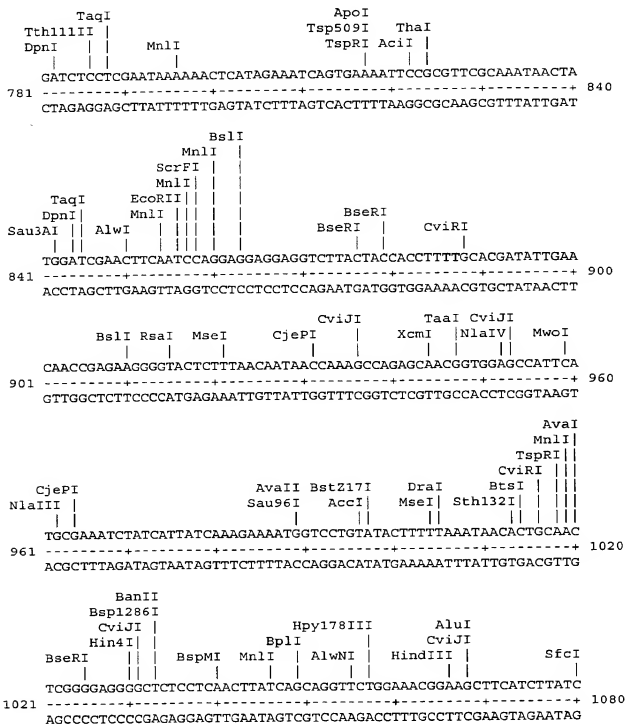


Fig. 24 (con't)



PCT/CA99/00992

BceI  
 NlaIII  
 NspI  
 SphI  
 MnlI  
 CviJI  
 HaeIII  
 Cac8I  
 Tth111II  
 PstI  
 CviRI  
 Hin4I  
 MseI  
 TGCAGATAATGGAGATATTATCTTTAACRATAATACGGCCTCCAAGCATGCCCTCAATCC  
 1081  
 ACGTCTATTACCTCTATAATAGAAATGTTATTATGCGGAGGTTCTGTACGGGAGTTAGG  
 1140  
 BsmFI  
 BanII  
 BscGI  
 Bsp1286I  
 MspI  
 CviJI  
 NciI  
 NlaIV  
 ScrFI  
 MnlI  
 MnlI  
 PleI  
 HinfI  
 TaqI  
 TCCATACAGAAACGCCATTCACTCGACTCCTAATATGAATCTGCAAAATAGGAGCCCCGTCC  
 1141  
 AGGTATGTCTTTGCGGTAAGTGAGCTGAGGATTACTTAGACGTTTATCTCTCGGCAGG  
 1200  
 BanII  
 BsiHKAII  
 Bsp1286I  
 SacI  
 AluI  
 CviJI  
 BsaXI  
 NlaIII  
 A1oI  
 PpiI  
 MnlI  
 TaqI  
 Sth132I  
 CviJI  
 Sth132I  
 Sau3AI  
 DpnI  
 AlwI  
 CGGCTATCGAGTGTCTGTTCTATGATCCCATAGAACATGAGCTCCCTTCCCTCTCCCAT  
 1201  
 GCCGATAGCTCACGACAAGATACTAGGGTATCTTGTACTCGAGGGAAGGAGGAAGGGGTA  
 1260  
 RsaI  
 NlaIII  
 NspI  
 BsrGI  
 TatiI  
 Tsp509I  
 NspV  
 MseI  
 TaqI  
 TaaI  
 RsaI  
 AflIII  
 BspLU11I  
 ACTCTTTAAATTCGAAACCGGTCATACAGGTACAGTTTTATTTTCAGGGGAACATGTACA  
 1261  
 TGAGAAATTAAGCTTTGGCCAGTATGTCATGTCAAATAAAGTCCCTTGTACATGT  
 1320

Fig. 24 (cont)

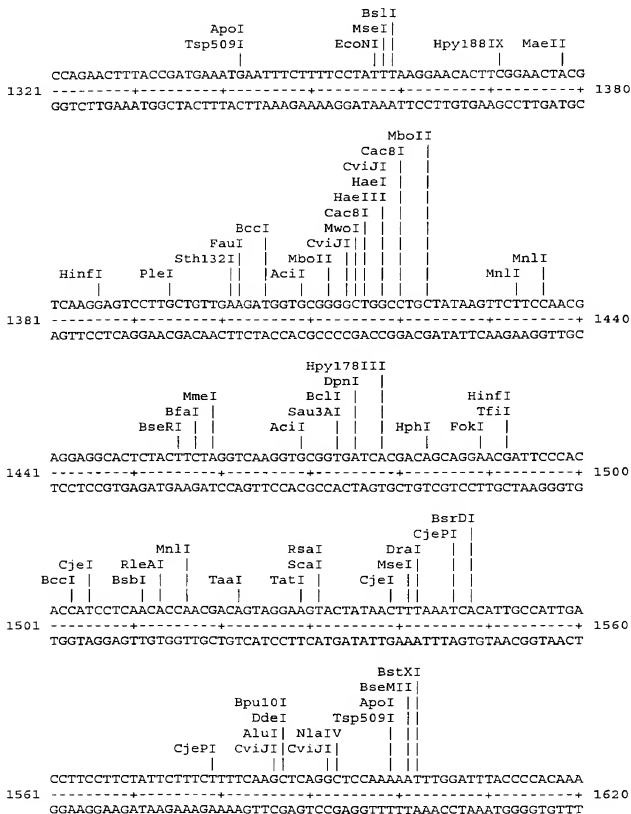




Fig. 24 (cont')

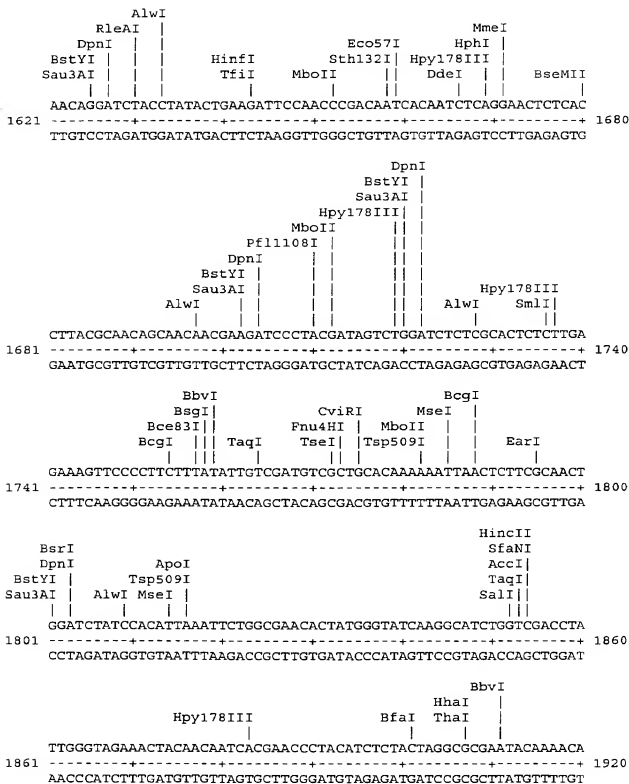
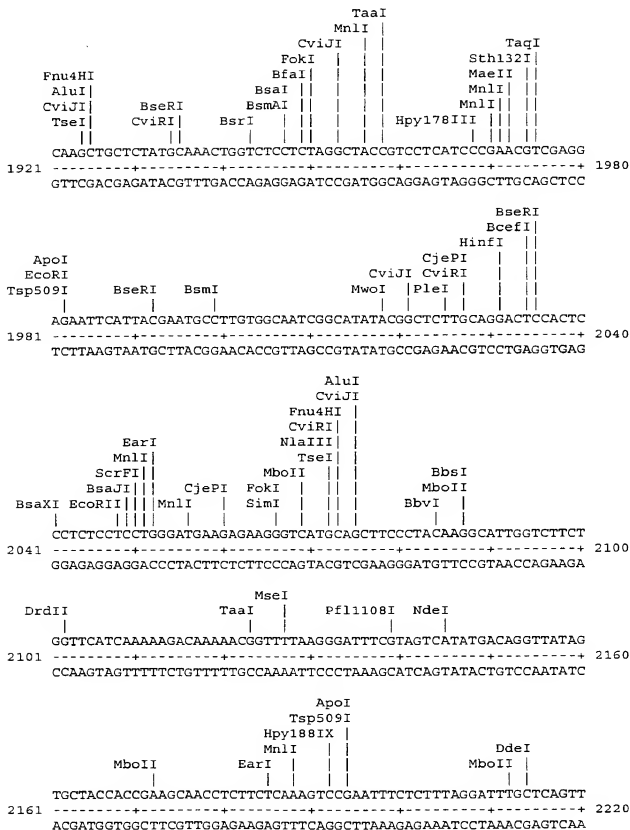


Fig. 24 (cont)



[illegible]

Fig. 24 (con't)

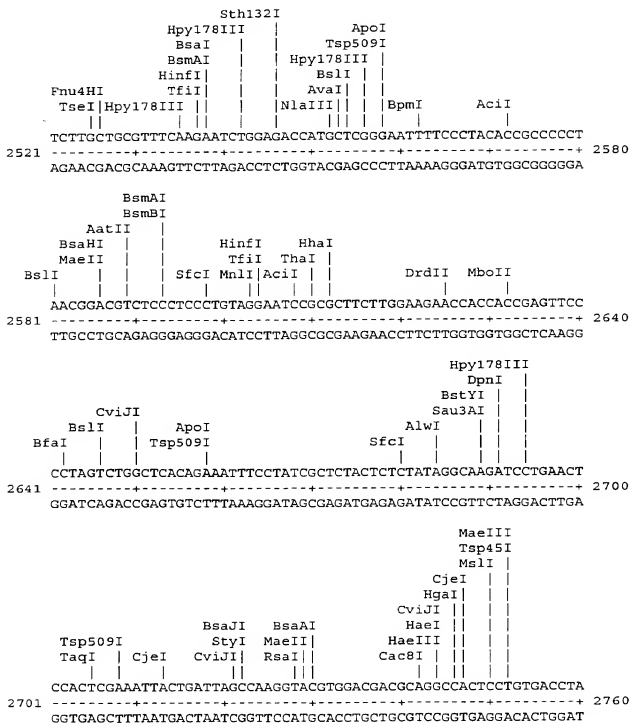
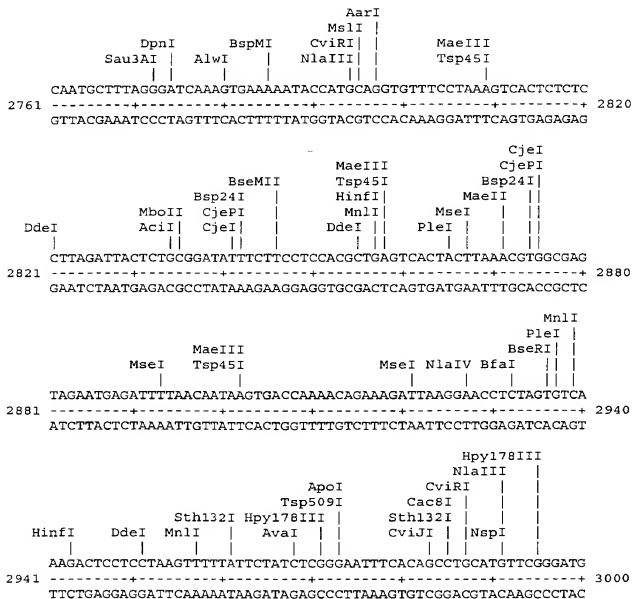


Fig. 24 (cont)



Title: CHLAMYDIA ANTIGENS AND  
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AND USES THEREOF

Inventor(s): Andrew D. MURDIN et al  
DOCKET NO.: 032931/0251

30446.052802  
09/830446

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PCT/CA99/00992

Figure 25:

```

cactgtggat gtgatattcg cagaacctcc cgtcaaatat actctagata taggaagcaa 60
attacgattt taaaccttat ttaacgacag ggttgaggc atg cct ctt tct ttc 114
                                Met Pro Leu Ser Phe
                                1                    5

aaa tct tca tct ttt tgt cta ctt gcc tgt tta tgt agt gca agt tgc 162
Lys Ser Ser Ser Phe Cys Leu Leu Ala Cys Leu Cys Ser Ala Ser Cys
                                10                    15                    20

gcg ttt gct gag act aga ctc gga ggg aac ttt gtt cct cca att acg 210
Ala Phe Ala Ala Glu Thr Arg Leu Gly Gly Asn Phe Val Pro Pro Ile Thr
                                25                    30                    35

aat cag ggt gaa gag atc tta ctc act tca gat ttt gtt tgt tca aac 258
Asn Gln Gly Glu Glu Ile Leu Leu Thr Ser Asp Phe Val Cys Ser Asn
                                40                    45                    50

ttc ttg ggg gcg agt ttt tca agt tcc ttt atc aat agt tcc agc aat 306
Phe Leu Gly Ala Ser Phe Ser Ser Ser Phe Ile Asn Ser Ser Ser Asn
                                55                    60                    65

ctc tcc tta tta ggg aag gcc ctt tcc tta acg ttt acc tct tgt caa 354
Leu Ser Leu Leu Gly Lys Gly Leu Ser Leu Thr Phe Thr Ser Cys Gln
                                70                    75                    80                    85

gct cct aca aat agt aac tat gcg cta ctt tct gcc gca gag act ctg 402
Ala Pro Thr Asn Ser Asn Tyr Ala Leu Leu Ser Ala Ala Glu Thr Leu
                                90                    95                    100

acc ttc aag aat ttt tct tct ata aac ttt aca ggg aac caa tcg aca 450
Thr Phe Lys Asn Phe Ser Ser Ile Asn Phe Thr Gly Asn Gln Ser Thr
                                105                    110                    115

gga ctt ggc gcc ctc atc tac gga aaa gat att gtt ttc caa tct atc 498
Gly Leu Gly Gly Leu Ile Tyr Gly Lys Asp Ile Val Phe Gln Ser Ile
                                120                    125                    130

aaa gat ttg atc ttc act acg aac cgt gtt gcc tat tct cca gca tct 546
Lys Asp Leu Ile Phe Thr Thr Asn Arg Val Ala Tyr Ser Pro Ala Ser
                                135                    140                    145

gta act acg tcg gca act ccc gca atc act aca gta act aca gga gcc 594
Val Thr Thr Ser Ala Thr Pro Ala Ile Thr Thr Val Thr Thr Gly Ala
                                150                    155                    160                    165

tct gct ctc caa cct aca gac tca ctc act gtc gaa aac ata tcc caa 642
Ser Ala Leu Gln Pro Thr Asp Ser Leu Thr Val Glu Asn Ile Ser Gln
Ser Ala Leu Gln Pro Thr Asp Ser Leu Thr Val Glu Asn Ile Ser Gln
                                170                    175                    180

tcg atc aag ttt ttt ggg aac ctt gcc aac ttc ggc tct gca att agc 690
Ser Ile Lys Phe Phe Gly Asn Leu Ala Asn Phe Gly Ser Ala Ile Ser
Ser Ile Lys Phe Phe Gly Asn Leu Ala Asn Phe Gly Ser Ala Ile Ser
                                185                    190                    195

```

Fig. 25 (con't)

agt tct ccc acg gca gtc gtt aaa ttc atc aat aac acc gct acc atg	738
Ser Ser Pro Thr Ala Val Val Lys Phe Ile Asn Asn Thr Ala Thr Met	
Ser Ser Pro Thr Ala Val Val Lys Phe Ile Asn Asn Thr Ala Thr Met	
200 205 210	
agc ttc tcc cat aac ttt act tcg tca gga ggc ggc gtg att tat gga	786
Ser Phe Ser His Asn Phe Thr Ser Ser Gly Gly Val Ile Tyr Gly	
Ser Phe Ser His Asn Phe Thr Ser Ser Gly Gly Val Ile Tyr Gly	
215 220 225	
gga agc tct ctc ctt ttt gaa aac aat tct gga tgc atc atc ttc acc	834
Gly Ser Ser Ser Leu Leu Phe Glu Asn Asn Ser Gly Cys Ile Ile Phe Thr	
Gly Ser Ser Ser Leu Leu Phe Glu Asn Asn Ser Gly Cys Ile Ile Phe Thr	
230 235 240 245	
gcc aac tcc tgt gtc aac agc tta aaa ggc gtc acc cct tca tca gga	882
Ala Asn Ser Cys Val Asn Ser Leu Lys Gly Val Thr Pro Ser Ser Gly	
Ala Asn Ser Cys Val Asn Ser Leu Lys Gly Val Thr Pro Ser Ser Gly	
250 255 260	
acc tat gct tta gga agt ggc gga gcc atc tgc atc cct acg gga act	930
Thr Tyr Ala Leu Gly Ser Gly Gly Ala Ile Cys Ile Pro Thr Gly Thr	
Thr Tyr Ala Leu Gly Ser Gly Gly Ala Ile Cys Ile Pro Thr Gly Thr	
265 270 275	
ttc gaa tta aaa aac aat cag ggg aag tgc acc ttc tct tat aat ggt	978
Phe Glu Leu Lys Asn Asn Gln Gly Lys Cys Thr Phe Ser Tyr Asn Gly	
Phe Glu Leu Lys Asn Asn Gln Gly Lys Cys Thr Phe Ser Tyr Asn Gly	
280 285 290	
aca cca aat gat gcg ggt gcg atc tac gcc gaa acc tgc aac atc gta	1026
Thr Pro Asn Asp Ala Gly Ala Ile Tyr Ala Glu Thr Cys Asn Ile Val	
Thr Pro Asn Asp Ala Gly Ala Ile Tyr Ala Glu Thr Cys Asn Ile Val	
295 300 305	
ggg aac cag ggt gcc ttg ctc cta gat agc aac act gca gcg aga aat	1074
Gly Asn Gln Gly Ala Leu Leu Leu Asp Ser Asn Thr Ala Ala Arg Asn	
Gly Asn Gln Gly Ala Leu Leu Leu Asp Ser Asn Thr Ala Ala Arg Asn	
310 315 320 325	
ggc gga gcc atc tgt gct aaa gtg ctc aat att caa gga cgc ggt cct	1122
Gly Gly Ala Ile Cys Ala Lys Val Leu Asn Ile Gln Gly Arg Gly Pro	
Gly Gly Ala Ile Cys Ala Lys Val Leu Asn Ile Gln Gly Arg Gly Pro	
330 335 340	
att gaa ttc tct aga aac cgc gcg gag aag ggt gga gct att ttc ata	1170
Ile Glu Phe Ser Arg Asn Arg Ala Glu Lys Gly Gly Ala Ile Phe Ile	
Ile Glu Phe Ser Arg Asn Arg Ala Glu Lys Gly Gly Ala Ile Phe Ile	
345 350 355	
ggc ccc tct gtt gga gac cct gcg aag caa aca tgc aca ctt acg att	1213
Gly Pro Ser Val Gly Asp Pro Ala Lys Gln Thr Ser Thr Leu Thr Ile	
Gly Pro Ser Val Gly Asp Pro Ala Lys Gln Thr Ser Thr Leu Thr Ile	
360 365 370	
ttg gct tcc gaa ggt gat att gcg ttc caa gga aac atg ctc aat aca	1266
Leu Ala Ser Glu Gly Asp Ile Ala Phe Gln Gly Asn Met Leu Asn Thr	
Leu Ala Ser Glu Gly Asp Ile Ala Phe Gln Gly Asn Met Leu Asn Thr	
375 380 385	

Fig. 25 (con't)

aaa cct gga atc cgc aat gcc atc act gta gaa gca ggg gga gag att Lys Pro Gly Ile Arg Asn Ala Ile Thr Val Glu Ala Gly Gly Glu Ile Lys Pro Gly Ile Arg Asn Ala Ile Thr Val Glu Ala Gly Gly Glu Ile 390 395 400 405	1314
gtg tct eta tct gca caa gga ggc tca cgt ctt gta ttt tat gat ccc Val Ser Leu Ser Ala Gln Gly Gly Ser Arg Leu Val Phe Tyr Asp Pro Val Ser Leu Ser Ala Gln Gly Gly Ser Arg Leu Val Phe Tyr Asp Pro 410 415 420	1362
att aca cat agc ctc cca acc aca agt cgg tct aat aaa gac att aca Ile Thr His Ser Leu Pro Thr Thr Ser Pro Ser Asn Lys Asp Ile Thr Ile Thr His Ser Leu Pro Thr Thr Ser Pro Ser Asn Lys Asp Ile Thr 425 430 435	1410
atc aac gct aat ggc gct tca gga tct gta gtc ttt aca agt aag gga Ile Asn Ala Asn Gly Ala Ser Gly Ser Val Val Phe Thr Ser Lys Gly Ile Asn Ala Asn Gly Ala Ser Gly Ser Val Val Phe Thr Ser Lys Gly 440 445 450	1458
ctc tcc tct aca gaa ctc ctg ttg cct gcc aac acg aca act ata ctt Leu Ser Ser Thr Glu Leu Leu Leu Pro Ala Asn Thr Thr Thr Ile Leu Leu Ser Ser Thr Glu Leu Leu Leu Pro Ala Asn Thr Thr Thr Ile Leu 455 460 465	1506
cta gga aca gtc aag atc gct agt gga gaa ctg aag att act gac aat Leu Gly Thr Val Lys Ile Ala Ser Gly Glu Leu Lys Ile Thr Asp Asn Leu Gly Thr Val Lys Ile Ala Ser Gly Glu Lys Ile Thr Asp Asn 470 475 480 485	1554
gcg gtt gtc aat gtt gct ggc ttc gct act cag ggc tca ggt cag ctt Ala Val Val Asn Val Ala Gly Phe Ala Thr Gln Gly Ser Gly Gln Leu Ala Val Val Asn Val Ala Gly Phe Ala Thr Gln Gly Ser Gly Gln Leu 490 495 500	1602
acc ctg ggc tct gga gga acc tta ggg ctg gca aca ccc acg gga gca Thr Leu Gly Ser Gly Gly Thr Leu Gly Leu Ala Thr Pro Thr Gly Ala Thr Leu Gly Ser Gly Gly Thr Leu Gly Leu Ala Thr Pro Thr Gly Ala 505 510 515	1650
cct gcc gct gta gac ttt acg att gga aag tta gca ttc gat cct ttt Pro Ala Ala Val Asp Phe Thr Ile Gly Lys Leu Ala Phe Asp Pro Phe Pro Ala Ala Val Asp Phe Thr Ile Gly Lys Leu Ala Phe Asp Pro Phe 520 525 530	1698
tcc ttc cta aaa aga gat ttt gtt tca gca tca gta aat gca ggc aca Ser Phe Leu Lys Arg Asp Phe Val Ser Ala Ser Val Asn Ala Gly Thr Ser Phe Leu Lys Arg Asp Phe Val Ser Ala Ser Val Asn Ala Gly Thr 535 540 545	1746
aaa aac gtc act tta aca gga ggc ctg gtt ctt gat gaa cat gac gtt Lys Asn Val Thr Leu Thr Gly Ala Leu Val Leu Asp Glu His Asp Val Lys Asn Val Thr Leu Thr Gly Ala Leu Val Leu Asp Glu His Asp Val 550 555 560 565	1794
aca gat ctt tat gat atg gtg tca tta caa tct cca gta gca att cct Thr Asp Leu Tyr Asp Met Val Ser Leu Gln Ser Pro Val Ala Ile Pro Thr Asp Leu Tyr Asp Met Val Ser Leu Gln Ser Pro Val Ala Ile Pro 570 575 580	1842



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Fig. 25 (con't)

atc gct gtt ttc aaa gga gca acc gtt act aag aca gga ttt cct gat	1890
Ile Ala Val Phe Lys Gly Ala Thr Val Thr Lys Thr Gly Phe Pro Asp	
Ile Ala Val Phe Lys Gly Ala Thr Val Thr Lys Thr Gly Phe Pro Asp	
585 590 595	
ggg gag att gcg act cca agc cac tac gcc tac caa gga aag tgg tcc	1938
Gly Glu Ile Ala Thr Pro Ser His Tyr Gly Tyr Gln Gly Lys Trp Ser	
Gly Glu Ile Ala Thr Pro Ser His Tyr Gly Tyr Gln Gly Lys Trp Ser	
600 605 610	
tac aca tgg tcc cgt ccc ctg tta att cca gct cct gat gga gga ttt	1986
Tyr Thr Trp Ser Arg Pro Leu Leu Ile Pro Ala Pro Asp Gly Gly Phe	
Tyr Thr Trp Ser Arg Pro Leu Leu Ile Pro Ala Pro Asp Gly Gly Phe	
615 620 625	
cct gga ggt ccc tct cct agc gca aat act ctc tat gct gta tgg aat	2034
Pro Gly Gly Pro Ser Pro Ser Ala Asn Thr Leu Tyr Ala Val Trp Asn	
Pro Gly Gly Pro Ser Pro Ser Ala Asn Thr Leu Tyr Ala Val Trp Asn	
630 635 640 645	
tca gac act ctc gtg cgt tct acc tat atc gaa gac ccc gag cgt tac	2082
Ser Asp Thr Leu Val Arg Ser Thr Tyr Ile Leu Asp Pro Glu Arg Tyr	
Ser Asp Thr Leu Val Arg Ser Thr Tyr Ile Leu Asp Pro Glu Arg Tyr	
650 655 660	
gga gaa att gtc agc aac agc tta tgg att tcc ttc tta gga aat cag	2130
Gly Glu Ile Val Ser Asn Ser Leu Trp Ile Ser Phe Leu Gly Asn Gln	
Gly Glu Ile Val Ser Asn Ser Leu Trp Ile Ser Phe Leu Gly Asn Gln	
665 670 675	
gca ttc tct gat att ctc caa gat gtt ctt ttg ata gat cat ccc ggg	2178
Ala Phe Ser Asp Ile Leu Gln Asp Val Leu Leu Ile Asp His Pro Gly	
Ala Phe Ser Asp Ile Leu Gln Asp Val Leu Leu Ile Asp His Pro Gly	
680 685 690	
ttg tcc ata acc gcg aaa gct tta gga gcc tat gtc gaa cac aca cca	2226
Leu Ser Ile Thr Ala Lys Ala Leu Gly Ala Tyr Val Glu His Thr Pro	
Leu Ser Ile Thr Ala Lys Ala Leu Gly Ala Tyr Val Glu His Thr Pro	
695 700 705	
aga caa gga cat gag gcc ttt tca ggt cgc tat gga gcc tac caa gct	2274
Arg Gln Gly His Glu Gly Phe Ser Gly Arg Tyr Gly Gly Tyr Gln Ala	
Arg Gln Gly His Glu Gly Phe Ser Gly Arg Tyr Gly Gly Tyr Gln Ala	
710 715 720 725	
gcg cta tct atg aac tac acg gac cac act acg tta gga ctt tct ttc	2322
Ala Leu Ser Met Asn Tyr Thr Asp His Thr Thr Leu Gly Leu Ser Phe	
Ala Leu Ser Met Asn Tyr Thr Asp His Thr Thr Leu Gly Leu Ser Phe	
730 735 740	
ggg cag ctt tat gga aaa act aac gcc aac ccc tac gat tca cgt tgc	2370
Gly Gln Leu Tyr Gly Lys Thr Asn Ala Asn Pro Tyr Asp Ser Arg Cys	
Gly Gln Leu Tyr Gly Lys Thr Asn Ala Asn Pro Tyr Asp Ser Arg Cys	
745 750 755	
tca gaa caa atg tat tta ctc tgg ttc ttt ggt caa ttc cct atc gtg	2418
Ser Glu Gln Met Tyr Leu Leu Ser Phe Phe Gly Gln Phe Pro Ile Val	
Ser Glu Gln Met Tyr Leu Leu Ser Phe Phe Gly Gln Phe Pro Ile Val	
760 765 770	

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Fig. 25 (con't)

act	caa	aag	agc	gag	gcc	tta	att	tcc	tgg	aaa	gca	gct	tat	ggt	tat	2466
Thr	Gln	Lys	Ser	Glu	Ala	Leu	Ile	Ser	Trp	Lys	Ala	Ala	Tyr	Gly	Tyr	
Thr	Gln	Lys	Ser	Glu	Ala	Leu	Ile	Ser	Trp	Lys	Ala	Ala	Tyr	Gly	Tyr	
775						780					785					
tcc	aaa	aat	cac	cta	aat	acc	acc	tac	ctc	aga	cct	gac	aaa	gct	cca	2514
Ser	Lys	Asn	His	Leu	Asn	Thr	Thr	Tyr	Leu	Arg	Pro	Asp	Lys	Ala	Pro	
Ser	Lys	Asn	His	Leu	Asn	Thr	Thr	Tyr	Leu	Arg	Pro	Asp	Lys	Ala	Pro	
790					795				800					805		
aaa	tct	caa	ggg	caa	tgg	cat	aac	aat	agt	tac	tat	ggt	ctt	att	tct	2562
Lys	Ser	Gln	Gly	Gln	Trp	His	Asn	Asn	Ser	Tyr	Tyr	Val	Leu	Ile	Ser	
Lys	Ser	Gln	Gly	Gln	Trp	His	Asn	Asn	Ser	Tyr	Tyr	Val	Leu	Ile	Ser	
				810				815					820			
gca	gaa	cat	cct	ttc	cta	aac	tgg	tgt	ctt	ctt	aca	aga	cct	ctg	gct	2610
Ala	Glu	His	Pro	Phe	Leu	Asn	Trp	Cys	Leu	Leu	Thr	Arg	Pro	Leu	Ala	
Ala	Glu	His	Pro	Phe	Leu	Asn	Trp	Cys	Leu	Leu	Thr	Arg	Pro	Leu	Ala	
				825				830					835			
caa	gct	tgg	gat	ctt	tca	ggg	ttt	att	tcc	gca	gaa	ttc	cta	ggt	ggt	2658
Gln	Ala	Trp	Asp	Leu	Ser	Gly	Phe	Ile	Ser	Ala	Glu	Phe	Leu	Gly	Gly	
Gln	Ala	Trp	Asp	Leu	Ser	Gly	Phe	Ile	Ser	Ala	Glu	Phe	Leu	Gly	Gly	
				840			845					850				
tgg	caa	agt	aag	ttc	aca	gaa	act	gga	gat	ctg	caa	cgt	agc	ttt	agt	2706
Trp	Gln	Ser	Lys	Phe	Thr	Glu	Thr	Gly	Asp	Leu	Gln	Arg	Ser	Phe	Ser	
Trp	Gln	Ser	Lys	Phe	Thr	Glu	Thr	Gly	Asp	Leu	Gln	Arg	Ser	Phe	Ser	
	855				860						865					
aga	ggt	aaa	ggg	tac	aat	gtt	tcc	cta	cgg	ata	gga	tgt	tct	tct	caa	2754
Arg	Gly	Lys	Gly	Tyr	Asn	Val	Ser	Leu	Pro	Ile	Gly	Cys	Ser	Ser	Gln	
Arg	Gly	Lys	Gly	Tyr	Asn	Val	Ser	Leu	Pro	Ile	Gly	Cys	Ser	Ser	Gln	
	870				875				880					885		
tgg	ttc	aca	cca	ttt	aag	aag	gct	cct	tct	aca	ctg	acc	atc	aaa	ctt	2802
Trp	Phe	Thr	Pro	Phe	Lys	Lys	Ala	Pro	Ser	Thr	Leu	Thr	Ile	Lys	Leu	
Trp	Phe	Thr	Pro	Phe	Lys	Lys	Ala	Pro	Ser	Thr	Leu	Thr	Ile	Lys	Leu	
				890					895					900		
gcc	tac	aag	cct	gat	atc	tat	cgt	gtc	aac	cct	cac	aat	att	gtg	act	2850
Ala	Tyr	Lys	Pro	Asp	Ile	Tyr	Arg	Val	Asn	Pro	His	Asn	Ile	Val	Thr	
Ala	Tyr	Lys	Pro	Asp	Ile	Tyr	Arg	Val	Asn	Pro	His	Asn	Ile	Val	Thr	
				905				910					915			
gtc	gtc	tca	aac	caa	gag	agc	act	tgc	atc	tca	gga	gca	aat	cta	cgc	2998
Val	Val	Ser	Asn	Gln	Glu	Ser	Thr	Ser	Ile	Ser	Gly	Ala	Asn	Leu	Arg	
Val	Val	Ser	Asn	Gln	Glu	Ser	Thr	Ser	Ile	Ser	Gly	Ala	Asn	Leu	Arg	
				920			925				930					
cgc	cac	ggg	ttg	ttt	gta	caa	atc	cat	gat	gta	gta	gat	ctc	acc	gag	2946
Arg	His	Gly	Leu	Phe	Val	Gln	Ile	His	Asp	Val	Val	Asp	Leu	Thr	Glu	
Arg	His	Gly	Leu	Phe	Val	Gln	Ile	His	Asp	Val	Val	Asp	Leu	Thr	Glu	
	935				940						945					

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Fig. 25 (con't)

gac	act	cag	gcc	ttt	cta	aac	tat	acc	ttt	gac	ggg	aaa	aat	gga	ttt	2994
Asp	Thr	Gln	Ala	Phe	Leu	Asn	Tyr	Thr	Phe	Asp	Gly	Lys	Asn	Gly	Phe	
Asp	Thr	Gln	Ala	Phe	Leu	Asn	Tyr	Thr	Phe	Asp	Gly	Lys	Asn	Gly	Phe	
950					955					960					965	
aca	aac	cac	cga	gtg	tct	aca	gga	cta	aaa	tcc	aca	ttt	taaaactcta			3043
Thr	Asn	His	Arg	Val	Ser	Thr	Gly	Leu	Lys	Ser	Thr	Phe				
Thr	Asn	His	Arg	Val	Ser	Thr	Gly	Leu	Lys	Ser	Thr	Phe				
				970						975						
agctctgctt	agagttttct	gtagcccccgg	tcgtctttaga	atcctctatc	cctcctcgaa											3103
gaacttagca	atgaaggcca	agattctcac	tctatgagaa	ccccccc												3150

Figure 26 (RY-47)

Restriction enzyme analysis of CPN100630

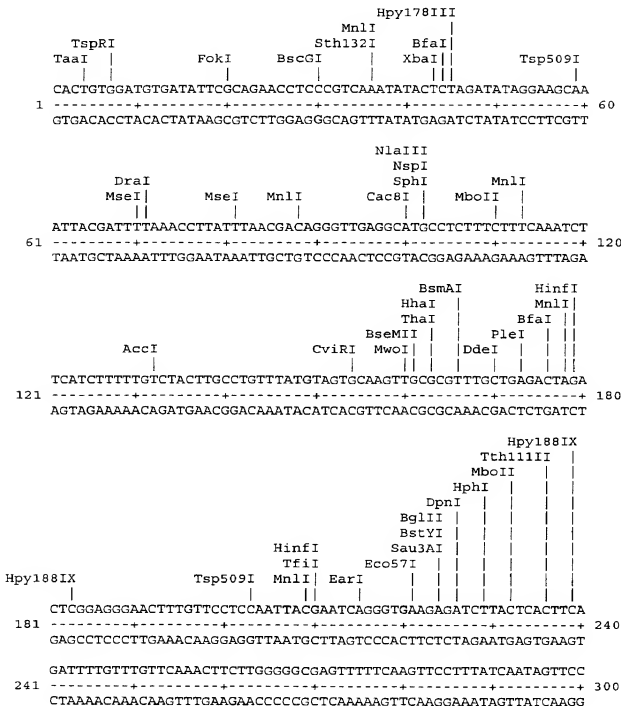


Fig. 26 (cont')



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Fig. 26 (con't)

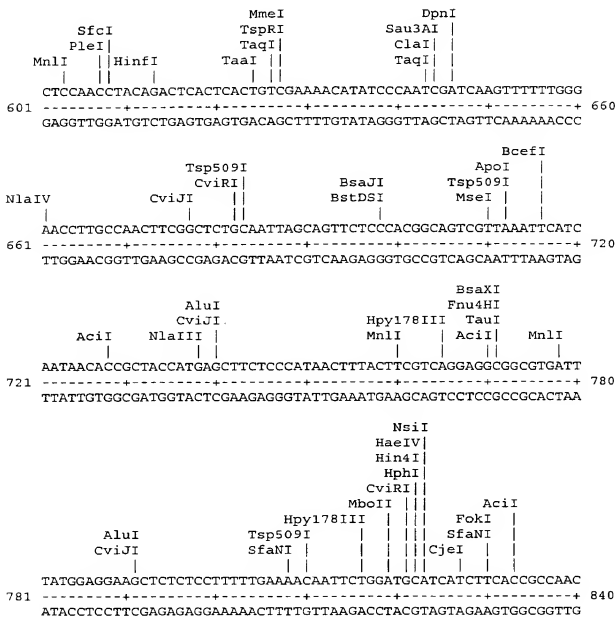


Fig. 26 (con't)

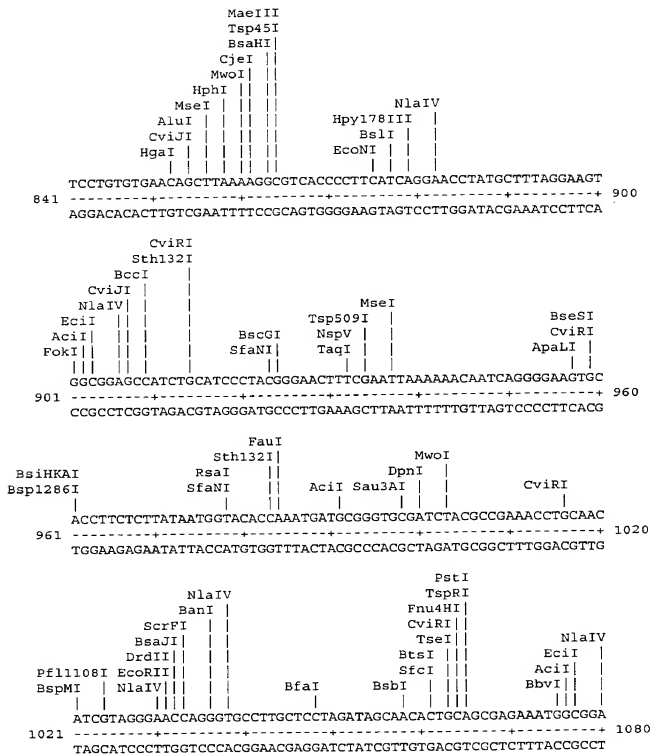


Fig. 26 (con't)

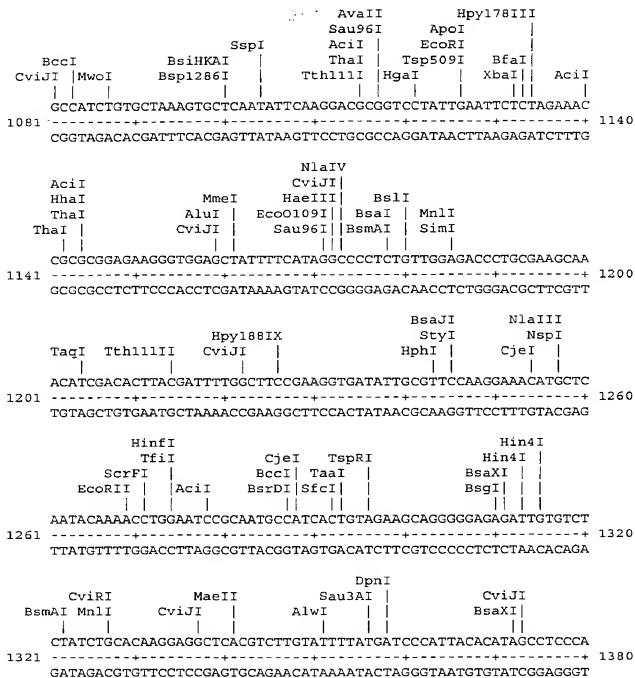
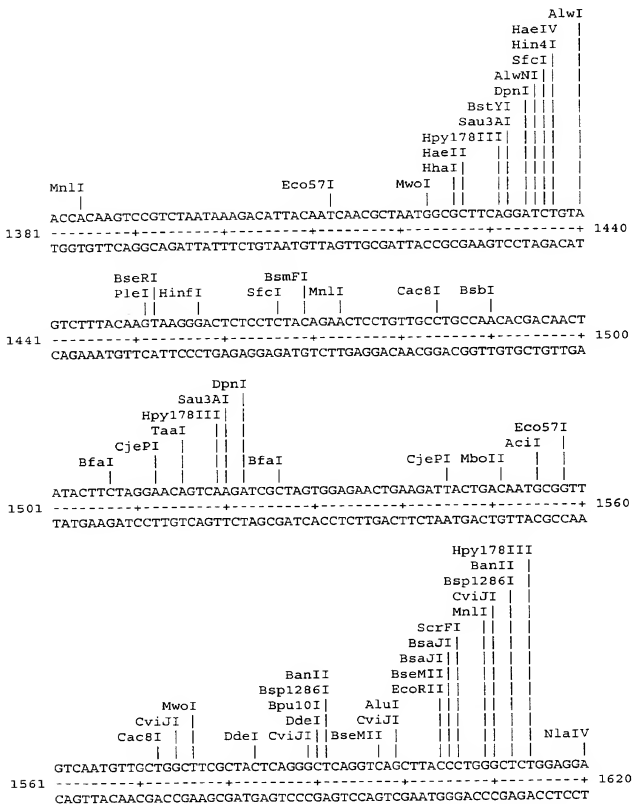




Fig. 26 (con't)



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[illegible]

Fig. 26 (con't)

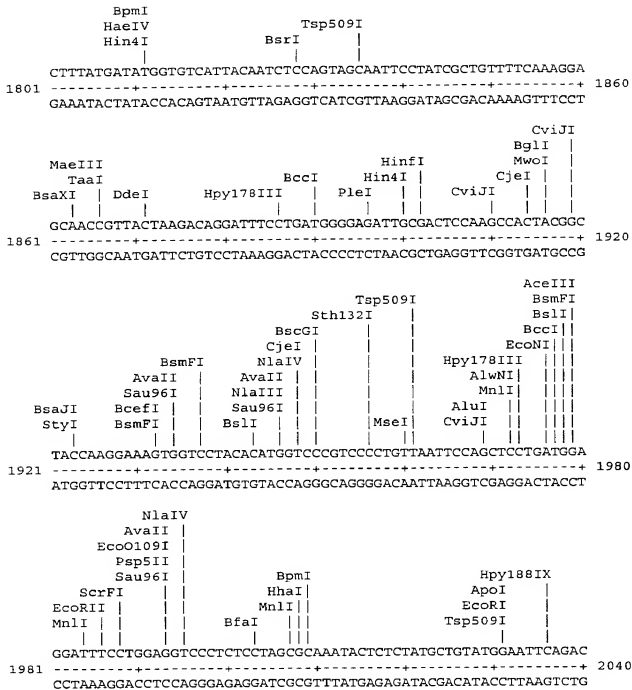


Fig. 26 (cont')

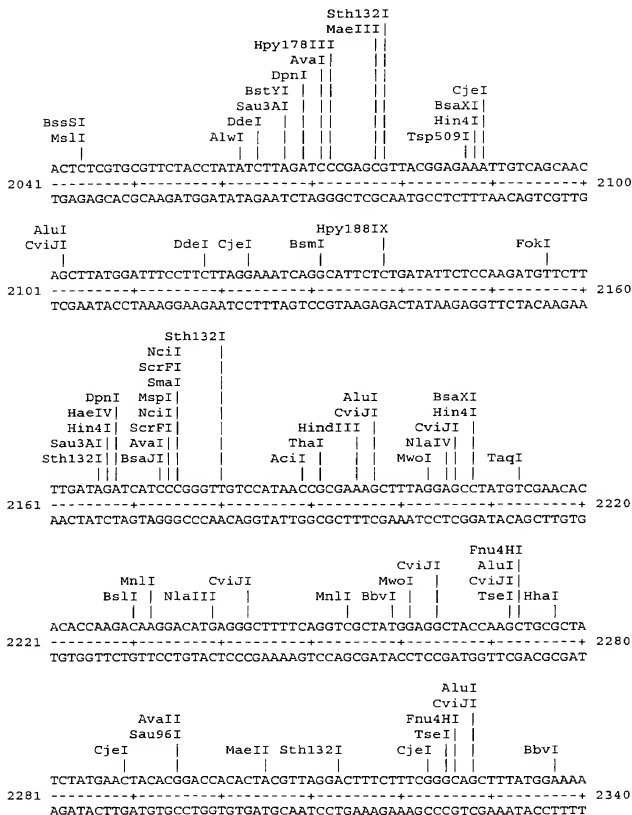
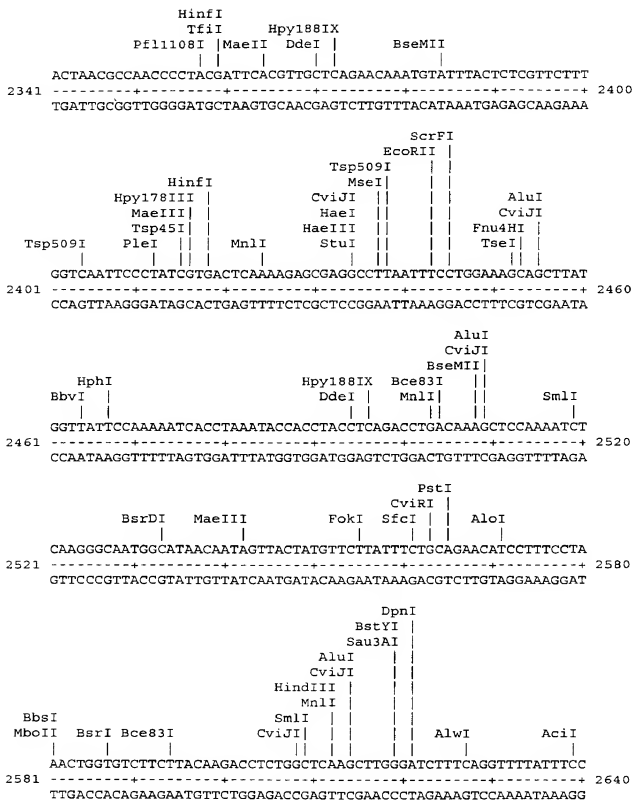


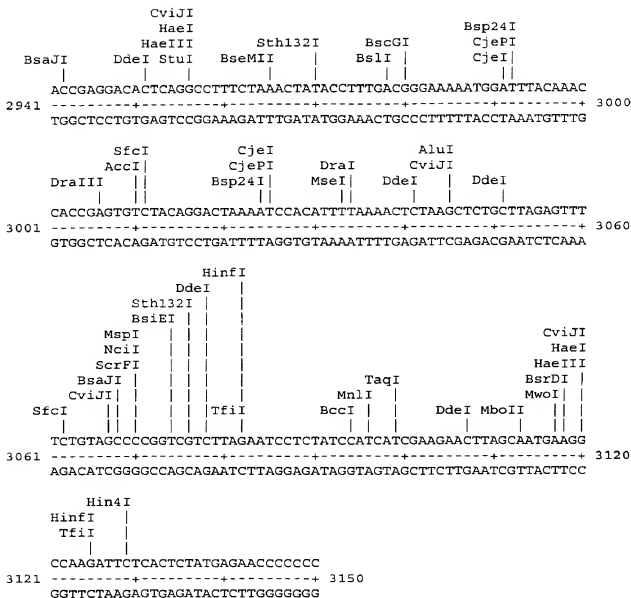
Fig. 26 (cont')



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BfaI  
 AvrII  
 BsaJI  
 ApoI  
 EcoRI  
 Tsp509I  
 StyI  
 CjeI  
 MaeIII  
 DpnI  
 BglII  
 BsrI  
 BstYI  
 Sau3AI  
 AlwNI  
 CviRI  
 AluI  
 CviJI  
 CjeI  
 2641  
 GCAGAAATTCCTAGGTGGTGGCAAAGTAAGTTCACAGAAACTGGAGATCTGCAACGTAGC  
 2700  
 CGTCTTAAGGATCCACCAACCGTTTCATTCAAGTGCTTTGACCTCTAGACGTTGCATCG  
 BpmI  
 MnlI  
 RsaI  
 MboII  
 FokI  
 DrdII  
 2701  
 TTTAGTAGAGSTAAGGGGTACAATGTTTCCTTACCGATAGGATGTTCTTCTCAATGGTTC  
 2760  
 AAATCATCTCCATTTCCCATGTTTACAAAGGGATGGCTATCTCTACAAGAAGAGTTACCAAG  
 MseI  
 NlaIV  
 CviJI  
 BccI  
 TspRI  
 CviJI  
 EcoRV  
 BsaBI  
 2761  
 ACACCATTTAAGAAGGCTCTCTTCTACACTGACCATCAAACCTGCCTACAAGCGCTGATATC  
 2820  
 TGTGGTAAATTCCTCCGAGGAAGATGTGACTGGTAGTTTGAACGGATGTTTCGGACTATAG  
 HincII  
 MaeIII  
 Tsp45I  
 MnlI  
 SspI  
 PshAI  
 TaaI  
 BsmAI  
 BsmBI  
 BsiHKAII  
 Bsp1286I  
 DdeI  
 DpnI  
 Sau3AI  
 TaqI  
 2821  
 TATCGTGTCAACCTCACAATATTGTGACTGTGCTCTCAAACCAAGAGAGCACTTCGATC  
 2880  
 ATAGCAGCAGTTGGGAGTGTTTATAACACTGACAGCAGAGTTTGGTCTCTCGTGAAGCTAG  
 BsaJI  
 BstDSI  
 Tth111III  
 AciI  
 Fnu4HI  
 BseMII  
 CjeI  
 TauI  
 TaaI  
 RsaI  
 BsrGI  
 TatI  
 NlaIII  
 HphI  
 MnlI  
 DpnI  
 BglII  
 BstYI  
 Sau3AI  
 Hpy178III  
 2881  
 TCAGGAGCAAATCTACGCCGCCACGGTTTGTGTGTACAAATCCATGATGTAGTAGATCTC  
 2940  
 AGTCCTCGTTTAGATGCGCGGTGCGAAACAAACATGTTTAGGTACTACATCATCTAGAG

Fig. 26 (con't)



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Figure 27: CPN100397

```
1 MKIPLRFLLI SLVPTLSMSN LLGAATTEEL SASNSFDGTT STTSFSSKTS
51 SATDGTNYVF KDSVVIVNVP KTGETQSTSC FKNDAAAGDL NFLGGGFSFT
101 FSNIDATTAS GAAIGSEAAK KTVTLQSFSA LSFLKSPAST VTNGLGAINV
151 KGNLSLLDND KVLIQDNFST GDGGAINCAG SLKIANNKSL SFIGNSSSTR
201 GGAIHTKNLT LSSGGETLFQ GNTAPTAAGK GGAIAIADSG TLSISGDSGD
251 IIFEGNTIGA TGTVSHSAID LGTSAKITAL RAAQGHITIY YDPITVTGST
301 SVADALNINS PDTGDNKEYT GTIVFSGEKL TEAEAKDEKN RTSKLLQNV
351 FKNGTVVLKG DVVLSANGFS QDANSKLIMD LGTSLVANTE SIELTNLEIN
401 IDSLRNGKKI KLSAATAQKD IRIDRPVVLA ISDESFYQNG FLNEDHSYDG
451 ILELDAGKDI VISADRSID AVQSPYGYQG KWTINWSTD DD KKATVSWAQ
501 SFNPTAEQEA PLVPNLLWGS FIDVRSFQNF IELGTEGAPY EKRFVWAGIS
551 NVLHRSGREN QKRFHRVSGG AVVGASTRMP GGDTLSELGFA QLFARDKDYF
601 MNTNFAKTYA GSLRLQHDAS LYSVVSILLG EGGLEILLP YVSKTLPCCF
651 YQQLSYGHTD HRMKTESLPP PPPTLSTDHT SWGGYVWAGE LGTRVAVENT
701 SGRGFFQEYT PFVKVQAVYA RQDSFVELGA ISRDFSDSHL YNLAIPLGIK
751 LEKRFAEQYY HVVAMYSFV CRSNPKCTTT LLNQGSSWKT KGSNLRQAG
801 IVQASGFRSL GAAAEFLGNF GFEWRGSSRS YNVDAGSKIK F
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Possible T cell epitope:

516 LLWGSFIDV

Possible B cell epitope:

554 HRSGRENQKRFHV



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Figure 28: CPN100421

1 MPPLNADDVL PRDHLSDGSF SDTYPDITTO AIILIFLALS PFLVMLLTSY  
51 LKIIITLVLL RNALGVQQT P PSQVLNGIAL ILSIYVMFPT GVAMYKDARK  
101 EIEANTIPOS LFTAEGAETV FVALNKSKEP LRSFLIRNTP KAQIQSFYKI  
151 SOKTFPSEIR AHLTASDPVI IIPAFIMGQI KNAFEIGVLI YLPFFVIDLV  
201 TANVLVAMQM MMLSPLSISL PLKLLLIVMV DGWTLLLQGL MISFK

Possible T cell epitope:

188 VLIYLPFFV

Possible B cell epitope:

125 NKSKEPLR

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Figure 29: CPN100422

1	MKFFSLIFKD	DDVSPNKKVL	SPEAFSAFLD	AKELLEKTKA	DSEAYVAETE
51	QKCAQIRQEA	KDQGFKEGSE	SWSKQIAFLE	EETKNLRIRV	REALVPLAIA
101	SVRKIIIGKEL	ELHPETIVSI	ISQALKELTQ	NKHIIISVNP	KDPLVVEKSR
151	PELKNIVEYA	DSLILTAKPD	VTPGGCIIET	EAGIINAQLD	VQLDALEKAF
201	STILKAKNPV	DEPSETSSST	DSSSLSDNDQD	KKE	

Possible T cell epitope:

163 LILTAKPDV

Possible B cell epitope:

226 SNDQDKKE

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Figure 30: CPN100424

1 MTLCCCTSCN SRSLLIVHGLP GREANEIVVL LVSKGVAAQK LPOAAAATAG  
51 AATEQMWDIA VPSAQITEAL AILNQAGLPR MKGTSLLDLF AKQGLVPEL  
101 QEKIRYQEG L SEQMASTIRK MDGVVDASVQ ISPTTENEDN LPLTASVYIK  
151 HRGVLDNPNS IMVSKIKRLI ASAVFGLVPE NVSVVSDRAA YSDITINGPW  
201 GLTEEIDYVS VWGIILAKSS LTKFRLIFYV LILILFVISC GLLWVIWKTH  
251 TLIMTMGGTK GFFNPPTYTK NALEAKKAEG AADKEKKED ADSQGSKNA  
301 ETSDKDSSDK DAFEGSNEIE GA

Possible T cell epitope:

201 GLTEEIDYV

Possible B cell epitope:

284 DKEKKEDADSQGSKNAETSDKDSSDKDAFEGSNEIE

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Figure 31: CPN100426

1 MTIRVRNLAY SVNKKKILDG VTFSLERGHI TLFVGKSGSG KTMILRALAG  
51 LVQPTOGDIW IEGEAPALVF QQPELFSHMT VLGNCNTHPOI HIKGRSTEEA  
101 REKAFELLHL LDIEEVAKNY PDQLSGGQKQ RVAIVRSLCM DKHTLLFDEP  
151 TSALDPPFATA SFRHLLLETLR DQELTVGLTT HDMQFVHSCL DRIYLLDQGT  
201 VAGVYDKRDG ELDSGHPLESLK YIHSQA

Possible T cell epitope:

145 LLFDEPTSA

Possible B cell epitope:

205 YDKRDGE

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Figure 32: CPN100508

1	MKRPFPTYLC	IIFYGSCASL	SLHAGLSFPE	VRGATAAVVH	ADSGKVIFYDK
51	DIDAVIYPAS	MTKIATALFI	LKHYPTVLDT	LIKVKQDAIA	SITPQAKKQS
101	GYRSPPHWLE	TDGSTIQLHL	REELLGWDLF	HALLVCSAND	AANVLAMACC
151	GSVEKPMDKL	NFFLKEEIGC	THTHFNNPHG	LHHFNHYTTT	RDLISIMRCA
201	LKEPPFRGVI	STTSYKIGAT	NLHGERILSP	TNKL L L PGST	YHYPPALGGK
251	TGTTKTAGKN	LIMAAEKNNR	LLVTIATGYS	GPVSDLYQDV	IALCETVFNE
301	PLLRKELVPP	SDCLQLEIAN	LGKLSCLPPE	GLYDYFYASE	DREPLSVSFI
351	AHADAFPIEQ	GDLLGHWVFP	DDEGKISSQ	PFIYAPCRFER	TIKPKWLYMK
401	RVFTSYRTYM	SITMLLMYFR	IRKHKRYKNL	KHYSKI	

Possible T cell epitope:

156 FMDKLNFFL

Possible B cell epitope:

422 RKHRKYKN

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Figure 33: CPN100515

1 MASNPILOIE DLSITLAKOR QQYPIVQSLS FTINEGQTLA IIGESGSGKS  
51 VSAHAILRLL PCPPFSVSGQ VNFQGHNLLT ASRSIQKKII GTEISMIFON  
101 PQASLNPVFT IEQQFREIIH THLALTAEVA KEKMLYALEE TGFHDPRCLCL  
151 NLYPHQLSGG MLQRICIAMA LLCSPKLLIA DEPTTALDVS VOYQIILQLLK  
201 TLQKKTGMSL LIITHNMGVV AETADDVLVL YAGRMVECAP AVQMFINPNSH  
251 PYTRDLLASR PSLQPQQLGS FNPPIGQPPH YTAFFSGCRY HPRCSKILNR  
301 CSAEAPETYP VREGHKVRVG CMTNFPQPL IQATSLTKHY YKRSFWFQOK  
351 TIASRPVDDV SFSLYSRRV GLIGESGSGK STLALALAGL LPLTSGFLT  
401 NGTPIKLHSK HGRHQLRSQV RLVFQNPQAS LNPRTILDS LGHSLLYHKL  
451 VPKEKVLATV REYLELVGLS EEFYFYPHQ LSGQQQQRVS IARALLGVVQ  
501 LIICDEIVSA LDLSIQAQIL NMLAELQKKL SLTYLFISHD LAVVRSFCTE  
551 VFIMYKGQIV EKGNTKRIFS DPQHPYTRML LNAQLPETPD QRQSKPIFQE  
601 YHKDSEESCS TGCYFYNRCP QKQEACKSEI IPNQGDAAHT YRCIH

Possible T cell epitope:

59 LLPCPPFSV

Possible B cell epitopes:

18 KQRQQY

587 ETPDQRQSK

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Figure 34: CPN100538

```
1  MPGIEKAATT  VAVPQDKSEE  EKVKERLTRK  ELTCEDLKN  GYTVNFEDIS
51 ILELLQFVSK  ISGTNFFVDS  NDLOFNVTIV  SHDPTSVDDL  STILLQVLKM
101 HDLKVVVEQGN NVLIYRNPHL  SKLSTVVTDS  SLKETCEAVV  VTRVFRLYRR
151 QPSAAVNIIQ  PLLSHDAIVS  ASEATRHVII  SDIAGNVDKV  SDLLAALDCP
201 GTSVDMTEYE  VKYANFAALV  SYCQDVLGTL  AEDDAFQMF  I QPGTNKIFVV
251 SSPRLANKAE  QLLKSLDVPE  MAHTLDDPAS  TALALGGTGT  TSPKSLRFFM
301 YKLKYONGEV  IANALQDIGY  NLYVTTAMDE  DFINTLNSIQ  WLEVNNNSIVI
351 IGNQGNVDRV  IGLLNLGLDL  PKQVYIEVLI  LDTSLEKSWD  FGVQWVALGD
401 EQSKVAYASG  LLNNTGIATP  TKATVPPGTP  NPGSIPLPTP  GQLTGFSMDL
451 NSSSAFGLGI  IGNVLSHGK  SFLTGLGGLS  ALDQDGDVTI  VLNPRIMAQD
501 TQQASFFVGQ  TVPYQTIKYY  IQETGTVTQN  IDYEDIGVNL  VVTSTVAPNN
551 VVTLQIEQTI  SELHSASGSL  TPVTDKTYAA  TRLOIPDGCF  LVMSGHIRDK
601 TTKVVSGVPL  LNSIPLIRGL  FSRTIDQRQK  RNIMMFIKPK  VISSFEEGTR
651 VTNKEGYRYN  WEADEGSMQV  APRHAPECQG  PPSLQAESDF  KIIEIEAQ
```

Possible T cell epitope:

50 SILELLQFV

Possible B cell epitopes:

15 QDKSEEEK

626 DQRQKRN

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Figure 35: CPN100557

```
1  MSRKDNEVSL ARSIFNILSG TFCSRITGIF REIAMATYFG ADPIVAAPFWL
51  GFRTVFFLRK ILGGLILEQA FIPHFELRA QSLDRAAPFF RRFSLIKGS
101 TIIFTLLIEA VLWVFFNNVE EGYDMILLT MILLPCGIFL MMVNVNGALL
151 HCONKFFGVC LAPVVVNIW IFFVIAARHS DPRERIIGLS VALVIGFFFE
201 WLITVPGVWK FLLEAKSPPO EHDSVRALLA PLSLGILTSS IFOLNLLSDI
251 CLARYVHEIG PLYLMYSLKI YQLPIHLFGF GVFTVLLPAI SRCVQREDHE
301 RGLKLMKFVL TLTMSVMIIM TAGLLLLALP GVRVLYEHGL FPQSAVYAIW
351 RVLRGYGASI IPMALAPLVS VLFYAQRQYA VPLFIGIGTA LANIVLSLVL
401 GRNVLKDVSG ISYATSITAW VOLYFLWYYS SKRLPMYSKL LWESIRRSIK
451 VMGTTMLACM ITLGLNILTQ TTYVIFLNPL TPLAWPLSSI TQAIAFLSE
501 SCIFLAPLEG FAKLLRVEDL INLASFEYWR GQGLLQROH VMQDTQN
```

Possible T cell epitope:

111 VLWVFFNNV

Possible B cell epitopes:

1 MSRKDNE  
295 QREDHERG



Title: CHLAMYDIA ANTIGENS AND  
CORRESPONDING DNA FRAGMENTS  
AND USES THEREOF

Inventor(s): Andrew D. MURDIN et al  
DOCKET NO.: 032931/0251

097/830446

PCT/CA99/00992

WO 00/24765

Figure 36: CPN100622

```
1  MKTSRNKQCK ITDPLSKSSF FVGALILGKT TILLNATPLS DYFDNQANQL
51  TTLFPLIDTL TMTPTYSHRA TLFQVRDDTN QDIVLDHONS IESWFENFSQ
101 DGGALSKCSL AITNTKNQIL FLNSFAIKRA GAMYVDGNFD LSENHSGGAI
151 SGNLSFPNAS NFADTCTGGA VLCSKNVTIS KMQGTAYFIN NKAKSSGGAI
201 QAAIINIKDN TGPCLFPNNA AGGTAGGALF ANACRIENNS OPIYFLNQS
251 GLGGAIRVHQ ECILTNTGTS VIFMNNFAME ADISANHSSG GAIYCISSCSI
301 KDNPGIAAFD NNTAARDGGA ICTQSLTIQD SGPVYFTNNQ GTWGGAIMLR
351 QDGACTLFAD QGDIIFYNNR HFKDTFSNHV SVNCTRNVSL TVGASQGHSA
401 TFYDPILQRY TIQNSIQKFN PNPEHLGTL FSSTYIPDTS TSRDDFISHF
451 RNHIGLYNGT LALEDRAEWK VYKFDQFGGT LRLGSRVFS TTDEEQSSSS
501 VGSVININNL AINLPSILGN RVAPKLWIRP TGSSAPYSED NNPIINLSGP
551 LSLLDDENLD PYDTADLAQP IAEVPLLYLL DVTAKHINTD NFYPEGLNTT
601 QHYGYQGVWS PYWIETITTS DTSSEDTVNT LHRQLYGDWT PTGYKVNPEN
651 KGDIALSAFW QSFHNLFATL RYQTQQQIA PTASGEATRL FVHQNSNNDNA
701 KGFHMEATGY SLGTTSENTAS NHSFGVNFQO LFSNLYESH S DNSVASHTTLT
751 VALQINNPNWL QERFSTSASL AYSYSNHHIK ASGYSKIQOT EGKCYSTTLG
801 AALSCSLSLQ WRSRPLHFTP FIQAIAVRSN QTAPOESGDK ARKFSVHKPL
851 YNLTVPLGIQ SAWESKFRLP TYWNIELAYQ PVLYQQNPEI NVSLESSGSS
901 WLLSGTTLAR NAIAPKGRNQ IFIPPKLSVF LDYQGSVSSS TTHYLHAGT
951 TFKF
```

Possible T cell epitope:

119 ILFLNSFAI

Possible B cell epitopes:

```
2  KTSRNKQ
647 NPENKG
694 QNSNNDK
```

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Figure 37: CPN100626

```
1  MQVFPKVTLS LDYSADISSS TLSHYLNVAS RMRFLTISDQ NRKIKEPLVS
51 KTPPKFLFYL GNFTACMFGM TPAVYSLQTD SLEKFALERD EEFRTSFPLL
101 DSLSTLTGFS PITTFVGNRH NSSQDIVLSN YKSIDNILL WTSAGGAVSC
151 NNFLLSNVED HAPFSKNLAI GTGGAIACOG ACTITKNRGP LIFFSNRGLN
201 NASTGGETRG GAIACNGDFT ISQNQGTFFYF VNNSVNNWGG ALSTNGHCRI
251 QSNRAPLLFF NNTAPSGGGA LRSENTTISD NTRPIYFKNN CGNNGGAIOT
301 SVTVAIKWNS GSVIFNNNTA LSGSINSNGG SGGAIYTTNL SIDDNPCTIL
351 FNNNYCIRDG GAICTQFLTI KNSGHVYFTN NQGNWGGALM LLQDSTCLLF
401 AEQGNIAFQN NEVFLTTFGR YNAIHCTPNS NLQLGANKGY TTAFFDPIEH
451 QHPTTNPLIF NPNANHQGTI LFSAYIPEA SDYENNFISS SKNTSELRNG
501 VLSIEDRAGW QFYKFTQKGG ILKLGHAAAI ATTANSETPS TSVGSQVIIN
551 NLAINLPSIL AKGKAPTLWI RPLQSSAPFT EDNNPITLTS GPLTLLNEEN
601 RDPYDSIDLS EPLQNIHLLS LSDVTARHIN TDNFHPESLN ATEHYGYQGI
651 WSPYVWETIT TTNNASIETA NTLYRALYAN WTPLGKYNP EYQGDLATTP
701 LWQSFHTMFS LLRSYNRTGD SDIERPFLEI QGIADGLFVH QNSIPGAPGF
751 RIQSTGYSIQ ASSETSLHOK ISLGFAQFFT RTKEIGSSNN VSAHNTVSSL
801 YVELPWFOEA FATSHSLAYG YGDHHLHAYI RHKKNRAEGT CYSHTTAAAI
851 GCSFPNQOKS YLHLSPFVQA IAIRSHQAF EIEGDNPRKF VSKPKPFYNL
901 LPLGIQGWQ SKFHVPTWT LELSYQFVLY QQNPOIGVTL LASGGSWDIL
951 GHNVVRNALG YKVHNTALF RSLDLFLDYQ GSVSSSTSTH HLQAGSTLKF
```

Possible T cell epitope:

56 FLFYLGNT

Possible B cell epitopes:

39 DQNRKIK  
597 NEENRDPYD

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Figure 38: CPN100628

```
1 MLLPFTFVLA NEGLQLPLET YITLSPEYQA APQVGFTHNO NQDLAIVGNH
51 NDFILDYKYY RSNCGALTCK NLLISENIGN VFPEKNVCPN SGGAIYAAQN
101 CTISKQNYA FTTNLVSDNP TATAGSLGG ALFAINCST NNLGGQTFPD
151 NLALNKGAL YTTNLSIKD NKGPIIIKQN RALNSDSLGG GIYSGNSLNI
201 EGNSGAIQIT SNSSGSGGGI FSTQTLTISS NKKLIEISEN SAFANNYGSN
251 FNPGGGGLTT TFCTILNRE GVLFNNOQSO SNGCAIHAKS IIKENGVPY
301 FLNNTATRG ALLNLSAGSG NGSFILSADN GDIIFNNNTA SKHALNPPYR
351 NAIHSTPNMN LQIGARPGYR VLFYDPIEH LPSSFPILFN FETGHTGTVL
401 FSGEHVQNF TDEMNFSSYL RNTSELROGV LAVEDGAGLA CYKFFQGGT
451 LLLGQGAVIT TAGTIPTPSS TPTTVGSTIT LNHIADLPS ILSFQAQAPK
501 IWIYPTKTGS TYTEDSNPTI TISGTLTLRN SNNEPDYDSL DLSHSLEKVP
551 LLYIVDVAQ KINSSQLDLS TLNSGEHYGY QGIWSTYWVE TTTITNPTSL
601 LGANTKHKLL YANWSPLGYR PHPERRGEFI TNALWQSAYT ALAGLHSLSS
651 WDEEKHGAAS LQIGILLVHQ KDKNGFKGFR SHMTGYSATT EATSSQSPNF
701 SLGFAOFFSK AKEHESQNST SSHHYFSGMC IAKYSLORVI RLSVSLAYMF
751 TSEHTHTMYQ GLLEGNSQGS FHNHTLAGAL SCVFLPQPHG ESLQIYPFIT
801 ALAIRGNLAA FOESGDHARE FSLHRPLTDV SLPVGIRASW KNHHRVPLVW
851 LTBISYRSTL YRQDPELHSH LLISQCTWTT QATPVTYNAL GIKVKNTMQV
901 FPKVTLSLDY SADISSSTLS HYLNVASRMR F
```

Possible T cell epitope:

1 MLLPFTFVL

Possible B cell epitopes:

```
38 HNQNO
619 YRPHERRG
669 HQDKNG
```

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Figure 39: CPN100630

1	MPLSPKSSSF	CLLACLCSAS	CAFAETRLGG	NFVPPITNOG	EEILLTSDFW
51	CSNFLGASFS	SSFINSSSNL	SLLGKGLSLT	FTSCQAPTN	NYALLSAAET
101	LTFKNFSSIN	FTGNQSTGLG	GLIYGKDIVF	QSIKDLIFT	NRVAYSPASV
151	TTSATPAITT	VTTGASALQP	TDSLTVENIS	QSIKFFGNLA	NFGSAISSSP
201	TAVVKFINNT	ATMSFSHNFT	SSGGGVYGG	SSLFENNNSG	CIIFTANSCV
251	NSLKGVTSS	GTVALGSGGA	ICIPTGTPEL	KNNQGGKCTFS	YNGTPNDAGA
301	IYAETCNIVG	NQGALLDSN	TAARNGGAIC	AKVLNIQGRG	PIEFSRNRAE
351	KGGAIFIGPS	VGDPKQSTST	LTLASEGDI	AFQGNMLNTK	PGIRNAITVE
401	AGGEIVLSLA	QGGSRLVFYD	PITHSLPTTS	PSNKDITINA	NGAGSGVVFT
451	SKGLSSTELL	LPANTTITILL	GTVKIASGEL	KITDNAVNVN	AGPATOGSGQ
501	LTLGSGGTGL	LATPTGAPAA	VDFTIGKLAF	DPFSFLKRDF	VSASVNAVTK
551	NVTLTGALVL	DEHPTDLYD	MVSLQSPVAI	PIAVFKGATV	TKTGFPDGEI
601	ATPSHYGYQG	KWSYTWSRPL	LIPAPNGGFP	GGPSPSANTL	YAVWNSDTLV
651	RSTYILDPER	YGEIVSNSLW	ISPLNGQAFS	DILQDVLID	HPGLSITAKA
701	LGAYVEHTR	QGHEOFSORY	GGYQAALSMN	YTDHTTLGLS	FGQLYGKTNA
751	NPYDSRCSEQ	MYLLSFFGQF	PIVTQKSEAL	ISWKAAYGYS	KNHNLNTTYLR
801	PDKAPKSQGG	WHNNSYYVLI	SAEHPFLNWC	LLTRPLAQAW	DLSCFTSAEF
851	LGGWQSKFTE	TGDLQRSFSR	GKGYNVSLPI	GCSSQWFTPF	KKAPSTLTIK
901	LAYKPDIVRV	NPHNIVTVVS	NQESTSISGA	NLRRHGLFVQ	IHDVVDLTED
951	TQAFNLNYTFD	GKNGFTNHRV	STGLKSTF		

Possible T cell epitope:

936 GLFVQIHVD

Possible B cell epitopes:

281 KNNQGGK  
345 SRNRAEK  
707 HTPRQGEH

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## IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

## COMBINED DECLARATION AND POWER OF ATTORNEY

As a below named inventor, I hereby declare that: my residence, post office address and citizenship are as stated below next to my name; that I verily believe that I am the original, first and sole inventor (if only one name is listed below) or a joint inventor (if plural inventors are named below) of the subject matter which is claimed and for which a patent is sought on the invention entitled:

## CHLAMYDIA ANTIGENS AND CORRESPONDING DNA FRAGMENTS AND USES THEREOF

the specification of which

- ☐ is attached hereto.
- ☒ was filed on April 27, 2001
- as U.S. Application Serial No. 09/830,446
- ☒ was filed on October 28, 1999
- as PCT International Application No. PCT/CA99/00992

and (if applicable) was amended on February 8, 2001

I hereby state that I have reviewed and understand the contents of the above identified specification, including the claims, as amended by any amendment referred to above.

I acknowledge the duty to disclose information known to me which is material to the examination of this application in accordance with Title 37, Code of Federal Regulations, §§1.56(a) and (b), which state:

- "(a) A patent by its very nature is affected with a public interest. The public interest is best served, and the most effective patent examination occurs when, at the time an application is being examined, the Office is aware of and evaluates the teachings of all information material to patentability. Each individual associated with the filing and prosecution of a patent application has a duty of candor and good faith in dealing with the Office, which includes a duty to disclose to the Office all information known to that individual to be material to patentability as defined in this section. The duty to disclose information exists with respect to each pending claim until the claim is cancelled or withdrawn from consideration, or the application becomes abandoned. Information material to the patentability that is cancelled or withdrawn from consideration need not be submitted if the information is not material to the patentability of any claim remaining under consideration in the application. There is no duty to submit information which is not material to the patentability of any existing claim. The duty to disclose all information known to be material to patentability is deemed to be satisfied if all information known to be material to patentability of any claim issued in a patent was cited by the Office or submitted to the Office in the manner prescribed by §§1.97(b)-(d) and 1.98. However, no patent will be granted on an application in connection with which fraud on the Office was practiced or attempted or the duty of disclosure was violated through bad faith or intentional misconduct. The Office encourages applicants to carefully examine:
- (1) prior art cited in search reports of a foreign patent office in a counterpart application,
  - (2) the closest information over which individuals associated with the filing or prosecution of a patent application believe any pending claim patentably defines, to make sure that any material information contained therein is disclosed to the Office.

- (b) Under this section, information is material to patentability when it is not cumulative to information already of record or being made of record in the application, and
- (1) It establishes, by itself or in combination with other information, a prima facie case of unpatentability of a claim; or
  - (2) It refutes, or is inconsistent with, a position the applicant takes in:
    - (i) Opposing an argument of unpatentability relied on by the Office, or
    - (ii) Asserting an argument of patentability.

A prima facie case of unpatentability is established when the information compels a conclusion that a claim is unpatentable under the preponderance of evidence, burden-of-proof standard, giving each term in the claim its broadest reasonable construction consistent with the specification, and before any consideration is given to evidence which may be submitted in an attempt to establish a contrary conclusion of patentability."

I hereby claim foreign priority benefits under 35 United States Code, §119 and/or §365 of any foreign application(s) for patent or inventor's certificate listed below and have also identified below any foreign application for patent or inventor's certificate filed by me or my assignee disclosing the subject matter claimed in this application and having a filing date (1) before that of the application on which priority is claimed, or (2) if no priority claimed, before the filing of this application:

**PRIOR FOREIGN APPLICATION(S)**

Number	Country	Filing Date (Day/Month/Year)	Date First Laid-open or Published	Date Patented or Granted	Priority Claimed?
--------	---------	---------------------------------	---	-----------------------------	----------------------

I hereby claim the benefit under 35 United States Code, §119(e) of any United States provisional application(s) listed below:

Application Number	Filing Date
60/106,034	October 28, 1998
60/106,044	October 28, 1998
60/106,039	October 28, 1998
60/106,042	October 28, 1998
60/106,087	October 29, 1998
60/106,072	October 29, 1998
60/106,073	October 29, 1998
60/106,074	October 29, 1998
60/106,589	November 2, 1998
60/107,034	November 2, 1998
60/107,035	November 2, 1998
60/106,587	November 2, 1998
60/106,588	November 2, 1998

I hereby claim the benefit under Title 35, United States Code, §120 of any United States application(s) listed below and, insofar as the subject matter of each of the claims of this application is not disclosed in the prior United States application in the manner provided by the first paragraph of Title 35, United States Code, §112, I acknowledge the duty to disclose information which is material to patentability as defined in Title 37, Code of Federal Regulations, §1.56(a) which became available between the filing date of the prior application and the national or PCT international filing date of this application:

PRIOR U.S. OR PCT APPLICATION(S)

<u>Application No.</u>	<u>Filing Date</u> (day/month/year)	<u>Status</u> (pending, abandoned, granted)
------------------------	--	--

I hereby declare that all statements made herein of my own knowledge are true and that all statements made on information and belief are believed to be true; and further that these statements were made with the knowledge that wilful false statements and the like so made are punishable by fine or imprisonment, or both, under Section 1001 of Title 18 of the United States Code and that such wilful false statements may jeopardize the validity of the application or any patent issued thereon.

I hereby appoint the following patent agents with full power of substitution, association and revocation to prosecute this application and/or international application and to transact all business in the Patent and Trademark Office connected therewith:

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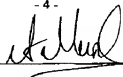
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(Middle)

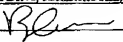
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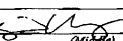
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## SEQUENCE LISTING

<110> MURDIN, Andrew D.; OOMEN, Raymond P; and WANG, Joe  
<120> Chlamydia antigens and corresponding DNA fragments and uses thereof  
10 <130> 77813-51  
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   Gly Thr Thr Ser Thr Thr Ser Phe Ser Ser Lys Thr Ser Ser Ala Thr
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	Thr Ala Leu Arg Ala Ala Gln Gly His Thr Ile Tyr Phe Tyr Asp Pro	
	280 285 290	
	att act gta aca gga tcg aca tct gtt gct gat gct ctc aat att aat	927
	Ile Thr Val Thr Gly Ser Thr Ser Val Ala Asp Ala Leu Asn Ile Asn	
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	gat gct gta caa tct ccg tat ggc tat cag gga aag tgg acg atc aat	1455
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	ggt act gaa ggt gct cct tac gaa aag aga ttt tgg gtt gca ggc att	1647
	Gly Thr Glu Gly Ala Pro Tyr Glu Lys Arg Phe Trp Val Ala Gly Ile	
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	Asp Tyr Phe Met Asn Thr Asn Phe Ala Lys Thr Tyr Ala Gly Ser Leu	
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	cgt ttg cag cac gat gct tcc cta tac tct gtg gtg agt atc ctt tta	1887
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	Gly Glu Gly Gly Leu Arg Glu Ile Leu Leu Pro Tyr Val Ser Lys Thr	
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	Arg Met Lys Thr Glu Ser Leu Pro Pro Pro Pro Pro Thr Leu Ser Thr	
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act cca ttt gta aaa gtc caa gct gtt tac gct cgc caa gat agc ttt 2175
Thr Pro Phe Val Lys Val Gln Ala Val Tyr Arg Gln Asp Ser Phe
710 715 720 725

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Met Pro Pro Leu Asn
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gtg agg aaa atc att ggg aag gaa ctc gaa tta cat cct gaa act att 451  
 Val Arg Lys Ile Ile Gly Lys Glu Leu Glu Leu His Pro Glu Thr Ile  
 105 110 115

gtc tct att att tct caa gca ttg aaa gag ctc aca caa aat aaa cat 499  
 Val Ser Ile Ile Ser Gln Ala Leu Lys Glu Leu Thr Gln Asn Lys His  
 120 125 130

atc att atc tct gtc aat ccc aaa gat tta cct ctt gtt gag aaa agt 547  
 Ile Ile Ile Ser Val Asn Pro Lys Asp Leu Pro Leu Val Glu Lys Ser  
 135 140 145

cgt cct gaa ctc aag aac atc gtg gag tat gct gac tcc tta att ctt 595  
 Arg Pro Glu Leu Lys Asn Ile Val Glu Tyr Ala Asp Ser Leu Ile Leu  
 150 155 160 165

aca gca aaa cct gat gtt act cct ggg ggt tgc att atc gag act gaa 643  
 Thr Ala Lys Pro Asp Val Thr Pro Gly Gly Cys Ile Ile Glu Thr Glu  
 170 175 180

gca ggg atc atc aat gcg cag ctt gat gta caa tta gat gcc tta gaa 691  
 Ala Gly Ile Ile Asn Ala Gln Leu Asp Val Gln Leu Asp Ala Leu Glu  
 185 190 195

aaa gct ttc tcg act ata cta aaa gcg aag aac cct gta gac gag cca 739  
 Lys Ala Phe Ser Thr Ile Leu Lys Ala Lys Asn Pro Val Asp Glu Pro  
 200 205 210

tct gag act tca tca tcc acg gat tct tct tct tta tct aat gat cag 787  
 Ser Glu Thr Ser Ser Ser Thr Asp Ser Ser Ser Leu Ser Asn Asp Gln  
 215 220 225

gat aag aaa gaa taaaggtatt cactattatg cgateccattt ttogattttc 839  
 Asp Lys Lys Glu  
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	Met Thr Leu Leu Cys	
	1 5	
	tgt aca agc tgt aac agc agg tct cta att gtg cac ggt ctt cct ggc	163
	Cys Thr Ser Cys Asn Ser Arg Ser Leu Ile Val His Gly Leu Pro Gly	
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	aga gaa gcg aat gag att gtg gtg ctt ttg gta agc aaa ggg gtg gct	211
	Arg Glu Ala Asn Glu Ile Val Val Leu Val Ser Lys Gly Val Ala	
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20	gca caa aaa ttg cct caa gct gca gcg gct aca gcc gga gca gct act	259
	Ala Gln Lys Leu Pro Gln Ala Ala Ala Thr Ala Gly Ala Ala Thr	
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	Glu Gln Met Trp Asp Ile Ala Val Pro Ser Ala Gln Ile Thr Glu Ala	
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30	ctt gcc att cta aat caa gcg ggt ctt cca cgt atg aaa ggg aca agc	355
	Leu Ala Ile Leu Asn Gln Ala Gly Leu Pro Arg Met Lys Gly Thr Ser	
	70 75 80 85	
	ctg tta gat ctt ttt gca aaa caa ggt ctt gtt cct tcc gag ctt cag	403
	Leu Leu Asp Leu Phe Ala Lys Gln Gly Leu Val Pro Ser Glu Leu Gln	
	90 95 100	
	gaa aaa atc cgt tat caa gaa ggc tta tca gaa cag atg gcc tct acg	451
	Glu Lys Ile Arg Tyr Gln Glu Gly Leu Ser Glu Gln Met Ala Ser Thr	
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	Ile Arg Lys Met Asp Gly Val Val Asp Ala Ser Val Gln Ile Ser Phe	
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	act aca gaa aat gaa gat aat ctt cct tta aca gcc tct gtg tat att	547
	Thr Thr Glu Asn Glu Asp Asn Leu Pro Leu Thr Ala Ser Val Tyr Ile	
	135 140 145	
50	aag cat cga ggg gtt ttg gac aat ccg aac agc att atg gtt tcc aaa	595
	Lys His Arg Gly Val Leu Asp Asn Pro Asn Ser Ile Met Val Ser Lys	
	150 155 160 165	
	att aag cgc ctt att gca agt gct gtt cca gga ctt gtg cca gag aac	643
	Ile Lys Arg Leu Ile Ala Ser Ala Val Pro Gly Leu Val Pro Glu Asn	
	170 175 180	
	gtc tct gta gtg agc gat cgc gca gct tat agt gat att aca att aat	691
	Val Ser Val Val Ser Asp Arg Ala Ala Tyr Ser Asp Ile Thr Ile Asn	
	185 190 195	
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ggt cct tgg gga tta aca gaa gaa atc gat tat gtt tct gtt tgg ggt 739  
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 200 205 210

att att ctt gcg aag tct tcg ctc acc aaa ttc cgt ctc att ttt tat 787  
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10 gtc ttg att ctc att tta ttt gtt att tct tgt ggt ctc ctt tgg gtc 835  
 Val Leu Ile Leu Ile Leu Phe Val Ile Ser Cys Gly Leu Leu Trp Val  
 230 235 240 245

att tgg aaa act cat act ctc att atg act atg gga ggt aca aaa ggg 883  
 Ile Trp Lys Thr His Thr Leu Ile Met Thr Met Gly Gly Thr Lys Gly  
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20 ttc ttc aac cct aca cca tat aca aag aat gcc ttg gaa gcc aag aaa 931  
 Phe Phe Asn Pro Thr Pro Tyr Thr Lys Asn Ala Leu Glu Ala Lys Lys  
 265 270 275

gcc gag gga gca gct gct gac aaa gag aaa aaa gaa gat gca gat tca 979  
 Ala Glu Gly Ala Ala Ala Asp Lys Glu Lys Lys Glu Asp Ala Asp Ser  
 280 285 290

cag ggg gaa agc aaa aat gcg gaa acc agt gat aaa gac tct agt gat 1027  
 Gln Gly Glu Ser Lys Asn Ala Glu Thr Ser Asp Lys Asp Ser Ser Asp  
 295 300 305

30 aaa gat gct cca gaa gga agc aat gaa att gag ggt gct tagtgactgc 1076  
 Lys Asp Ala Pro Glu Gly Ser Asn Glu Ile Glu Gly Ala  
 310 315 320

caaacactttt ggaactctag acatcttgat gaagcactcc aaggaagatg acctctccag 1136  
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ttttctgta tttctaggtt atcagaaaag agaaggagtt atg aca att aga gtc 115  
 Met Thr Ile Arg Val  
 1 5

10 cga aac ctt gcc tac tct gta aat aag aaa aag att cta gat ggt gta 163  
 Arg Asn Leu Ala Tyr Ser Val Asn Lys Lys Lys Ile Leu Asp Gly Val  
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act ttt tct tta gag cga ggg cac att aca ctg ttt gtt ggg aag agt 211  
 Thr Phe Ser Leu Glu Arg Gly His Ile Thr Leu Phe Val Gly Lys Ser  
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ggg tca gga aaa aca atg att tta cgt gct ttg gcg ggc tta gtc cag 259  
 Gly Ser Gly Lys Thr Met Ile Leu Arg Ala Leu Ala Gly Leu Val Gln  
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ccc act caa gga gat att tgg att gaa ggg gag gct cca gct cta gtt 307  
 Pro Thr Gln Gly Asp Ile Trp Ile Glu Gly Glu Ala Pro Ala Leu Val  
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ttc caa caa ccc gag tta ttt tcc cat atg aca gta tta gga aat tgc 355  
 Phe Gln Gln Pro Glu Leu Phe Ser His Met Thr Val Leu Gly Asn Cys  
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30 acc cat cca caa atc cat atc aag ggt cgt agt acc gaa gaa gct cga 403  
 Thr His Pro Gln Ile His Ile Lys Gly Arg Ser Thr Glu Glu Ala Arg  
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gaa aag gcg ttc gag ctt tta cat ttg ttg gat att gaa gag gtt gct 451  
 Glu Lys Ala Phe Glu Leu Leu His Leu Leu Asp Ile Glu Glu Val Ala  
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 Lys Asn Tyr Pro Asp Gln Leu Ser Gly Gly Gln Lys Gln Arg Val Ala  
 120 125 130

att gta cgt tct tta tgt atg gat aaa cat aca tta ctt ttt gat gaa 547  
 Ile Val Arg Ser Leu Cys Met Asp Lys His Thr Leu Leu Phe Asp Glu  
 135 140 145

cct aca tcg gct tta gat cct ttt gct acg gca tcg ttc cga cat ctt 595  
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50 tta gaa aca ctt cga gac cag gaa ctg act gta ggg tta act act cat 643  
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 170 175 180

gac atg caa ttt gtt cat agt tgt ttg gat cgt atc tat ctt ata gat 691  
 Asp Met Gln Phe Val His Ser Cys Leu Asp Arg Ile Tyr Leu Ile Asp  
 185 190 195

60 caa gga act gtt gcg ggg gtc tat gac aag cgt gac gga gag ctc gat 739  
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 200 205 210

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tct ggt cat cca tta tgc aaa tat atc cac tct gct caa taggactaca 788  
 Ser Gly His Pro Leu Ser Lys Tyr Ile His Ser Ala Gln  
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 tg 850

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 Met Lys Arg Pro Phe  
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ttt acc tat cta tgc atc atc ttc tac gga tct tgt gca tgc tta tct 163  
 Phe Thr Tyr Leu Cys Ile Ile Phe Tyr Gly Ser Cys Ala Ser Leu Ser  
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tta cat gca gga ctc tct ttc cca gaa gta cgt gga gct acg gct gct 211  
 Leu His Ala Gly Leu Ser Phe Pro Glu Val Arg Gly Ala Thr Ala Ala  
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gtt gtc cat gcc gac tct ggg aag gta ttc tat gat aaa gac ata gat 259  
 Val Val His Ala Asp Ser Gly Lys Val Phe Tyr Asp Lys Asp Ile Asp  
 40 45 50

gct gta atc tat cct gcc agc atg acg aaa atc gca act gcc ctc ttt 307  
 Ala Val Ile Tyr Pro Ala Ser Met Thr Lys Ile Ala Thr Ala Leu Phe  
 55 60 65

atc cta aag cac tat ccc aca gtc ctc gat act ctc atc aaa gtc aaa 355  
 Ile Leu Lys His Tyr Pro Thr Val Leu Asp Thr Leu Ile Lys Val Lys  
 70 75 80 85

60



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	Gln Asp Ala Ile Ala Ser Ile Thr Pro Gln Ala Lys Lys Gln Ser Gly	
	90 95 100	
	tat cgt agt cct ccc cac tgg tta gaa act gat gga tct aca ata cag	451
	Tyr Arg Ser Pro His Trp Leu Glu Thr Asp Gly Ser Thr Ile Gln	
	105 110 115	
10	ctc cat ctt cga gaa gag ctt tta ggg tgg gac ctg ttc cac gcc tta	499
	Leu His Leu Arg Glu Glu Leu Leu Gly Trp Asp Leu Phe His Ala Leu	
	120 125 130	
	ctg gtc tgt tct gct aat gat gct gcg aat gtc tta gct atg gca tgt	547
	Leu Val Cys Ser Ala Asn Asp Ala Ala Asn Val Leu Ala Met Ala Cys	
	135 140 145	
20	tgc gga tct gta gag aag ttt atg gat aag ctg aac ttc ttc tta aaa	595
	Cys Gly Ser Val Glu Lys Phe Met Asp Lys Leu Asn Phe Phe Leu Lys	
	150 155 160	
	gaa gaa atc ggc tgc act cat acc cat ttt aat aat ccc cat ggg tta	643
	Glu Glu Ile Gly Cys Thr His Thr His Phe Asn Asn Pro His Gly Leu	
	170 175 180	
	cat cat ccg aat cac tat act aca acc cgt gat ctt att agc atc atg	691
	His His Pro Asn His Tyr Thr Thr Thr Arg Asp Leu Ile Ser Ile Met	
	185 190 195	
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	Arg Cys Ala Leu Lys Glu Pro Pro Phe Arg Gly Val Ile Ser Thr Thr	
	200 205 210	
	agc tat aaa ata ggg gct aca aac ctg cat ggc gaa cgg atc cta tcc	787
	Ser Tyr Lys Ile Gly Ala Thr Asn Leu His Gly Glu Arg Ile Leu Ser	
	215 220 225	
40	cca aca aac aaa ttg ctt ctt cct ggg tct acc tac cac tat ccc cca	835
	Pro Thr Asn Lys Leu Leu Leu Pro Gly Ser Thr Tyr His Tyr Pro Pro	
	230 235 240 245	
	gct tta gga ggg aaa aca ggg acc acc aag act gca ggg aaa aat cta	883
	Ala Leu Gly Gly Lys Thr Thr Gly Thr Thr Ala Gly Lys Asn Leu	
	250 255 260	
	att atg gct gct gaa aaa aat aac cgc ctc ttg gta acg atc gca acg	931
	Ile Met Ala Ala Glu Lys Asn Asn Arg Leu Leu Val Thr Ile Ala Thr	
	265 270 275	
50	ggc tat tcg ggt cct gtg agt gat ctc tac caa gat gtc att gct cta	979
	Gly Tyr Ser Gly Pro Val Ser Asp Leu Tyr Gln Asp Val Ile Ala Leu	
	280 285 290	
	tgt gaa acg gta ttt aac gag ccg cta tta aga aaa gag ctc gtc ccc	1027
	Cys Glu Thr Val Phe Asn Glu Pro Leu Leu Arg Lys Glu Leu Val Pro	
	295 300 305	
60	ccc tcc gac tgt ctc caa tta gaa ata gcg aat ctt ggg aag ctt tct	1075
	Pro Ser Asp Cys Leu Gln Leu Glu Ile Ala Asn Leu Gly Lys Leu Ser	
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Cys Pro Leu Pro Glu Gly Leu Tyr Tyr Asp Phe Tyr Ala Ser Glu Asp
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cgc gaa cct ctt tct gta tct ttt att gca cat gcg gac gcc ttc cct 1171
Arg Glu Pro Leu Ser Val Ser Phe Ile Ala His Ala Asp Ala Phe Pro
          345          350          355

att gaa caa gga gat ctt ctt ggt cat tgg gtt ttt tat gac gat gaa 1219
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ggc aag aaa att tct tcc cag cct ttc tat gcc cct tgt cgt ttt gag 1267
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Tyr Arg Thr Tyr Met Ser Ile Thr Met Leu Leu Met Tyr Phe Arg Ile
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cgc aag cac cgc aag tat aaa aat tta aaa cac tat tct aaa atc 1408
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	Ile Leu Gln Ile Glu Asp Leu Ser Ile Thr Leu Ala Lys Gln Arg Gln	
	10 10 15 20	
	cag tac ccc atc gtc caa tct tta tcg ttt act atc aat gaa gga caa	211
	Gln Tyr Pro Ile Val Gln Ser Leu Ser Phe Thr Ile Asn Glu Gly Gln	
	25 30 35	
	acc tta gca atc att gga gaa tca gga tca gga aaa tct gtc tct gcg	259
	Thr Leu Ala Ile Ile Gly Glu Ser Gly Ser Gly Lys Ser Val Ser Ala	
	40 45 50	
	cat gca atc ctt cga tta ctt cct tgc ccc cca ttt tct gtt tct ggc	307
	His Ala Ile Leu Arg Leu Leu Pro Cys Pro Pro Phe Ser Val Ser Gly	
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	Gln Val Asn Phe Gln Gly His Asn Leu Leu Thr Ala Ser Arg Ser Ile	
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	caa aaa aag att ata ggg aca gaa att tct atg atc ttt caa aac ccg	403
	Gln Lys Lys Ile Ile Gly Thr Glu Ile Ser Met Ile Phe Gln Asn Pro	
	90 95 100	
	caa gca tct cta aac ccc gtg ttt act att gaa cag cag ttt cga gaa	451
	Gln Ala Ser Leu Asn Pro Val Phe Thr Ile Glu Gln Gln Phe Arg Glu	
	105 110 115	
	att att cat acc cac cta gcc tta act gca gaa gtt gct aaa gaa aag	499
	Ile Ile His Thr His Leu Ala Leu Thr Ala Glu Val Ala Lys Glu Lys	
	120 125 130	
	atg tta tac gct ctt gaa gaa aca ggg ttt cat gat ccc agg ctg tgc	547
	Met Leu Tyr Ala Leu Glu Thr Gly Phe His Asp Pro Arg Leu Cys	
	135 140 145	
	ttg aat ctc tac ccc cac caa ctc tct gga ggg atg ctt caa aga att	595
	Leu Asn Leu Tyr Pro His Gln Leu Ser Gly Gly Met Leu Gln Arg Ile	
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	tgc att gcc atg gcg ctc ctc tgt tct cct aaa ctt ctt att gct gat	643
	Cys Ile Ala Met Ala Leu Leu Cys Ser Pro Lys Leu Leu Ile Ala Asp	
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	gaa cct acg act gct tta gat gtt tct gtt cag tat cag att cta caa	691
	Glu Pro Thr Thr Ala Leu Asp Val Ser Val Gln Tyr Gln Ile Leu Gln	
	185 190 195	
	tta cta aaa aca cta cag aaa aaa acg gga atg agc ctt ctt att att	739
	Leu Leu Lys Thr Leu Gln Lys Lys Thr Gly Met Ser Leu Leu Ile Ile	
	200 205 210	
	acc cat aat atg gga gtc gtt gca gaa act gct gat gac gtg ctc gtg	787
	Thr His Asn Met Gly Val Val Ala Glu Thr Ala Asp Asp Val Leu Val	
	215 220 225	

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	His	Asn	Pro	Ser	His	Pro	Tyr	Thr	Arg	Asp	Leu	Leu	Ala	Ser	Arg	Pro	
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	Ser	Leu	Gln	Pro	Gln	Gln	Leu	Gly	Ser	Phe	Asn	Pro	Ile	Tyr	Gly	Gln	
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	ccc	cca	cac	tac	acg	gcc	ttt	ccc	tcg	gga	tgt	cgc	tat	cac	cct	aga	979
	Pro	Pro	His	Tyr	Thr	Ala	Phe	Pro	Ser	Gly	Cys	Arg	Tyr	His	Pro	Arg	
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	Cys	Ser	Lys	Ile	Leu	Asn	Arg	Cys	Ser	Ala	Glu	Ala	Pro	Glu	Ile	Tyr	
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	ccg	gta	cgc	gaa	ggg	cac	aaa	gta	agg	gtt	ggc	tgt	atg	acg	act	aat	1075
	Pro	Val	Arg	Glu	Gly	His	Lys	Val	Arg	Val	Gly	Cys	Met	Thr	Thr	Asn	
	310					315					320					325	
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	Phe	Pro	Gln	Pro	Leu	Ile	Gln	Ala	Thr	Ser	Leu	Thr	Lys	His	Tyr	Tyr	
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	Lys	Arg	Ser	Phe	Trp	Phe	Gln	Gly	Lys	Thr	Ile	Ala	Ser	Arg	Pro	Val	
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	gac	gac	gtc	tct	ttt	tca	cta	tac	tcc	aga	cgt	gct	gtc	gga	ctt	att	1219
	Asp	Asp	Val	Ser	Phe	Ser	Leu	Tyr	Ser	Arg	Arg	Ala	Val	Gly	Leu	Ile	
			360					365					370				
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	Gly	Glu	Ser	Gly	Ser	Gly	Lys	Ser	Thr	Leu	Ala	Leu	Ala	Leu	Ala	Gly	
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	ctc	cta	cct	ctc	acc	tct	ggg	ttc	tta	act	ttt	aac	ggc	acc	cca	atc	1315
	Leu	Leu	Pro	Leu	Thr	Ser	Gly	Phe	Leu	Thr	Phe	Asn	Gly	Thr	Pro	Ile	
			390			395				400					405		
	aag	ttg	cat	tct	aaa	cac	gga	cgc	cat	caa	tta	cga	tct	caa	gta	cgg	1363
	Lys	Leu	His	Ser	Lys	His	Gly	Arg	His	Gln	Leu	Arg	Ser	Gln	Val	Arg	
					410				415						420		
50	ttg	gtc	ttt	caa	aat	cca	caa	gct	tca	tta	aac	ccg	cga	aaa	act	atc	1411
	Leu	Val	Phe	Gln	Asn	Pro	Gln	Ala	Ser	Leu	Asn	Pro	Arg	Lys	Thr	Ile	
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	Leu	Asp	Ser	Leu	Gly	His	Ser	Leu	Leu	Tyr	His	Lys	Leu	Val	Pro	Lys	
			440				445						450				
60	gaa	aaa	gta	cta	gca	acg	gta	agg	gaa	tat	tta	gaa	ttg	gta	ggg	tta	1507
	Glu	Lys	Val	Leu	Ala	Thr	Val	Arg	Glu	Tyr	Leu	Glu	Leu	Val	Gly	Leu	
		455					460					465					

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tct gag gag tat ttt tat cgt tat cct cac cag ctt tct gga gga caa 1555  
 Ser Glu Glu Tyr Phe Tyr Arg Tyr Pro His Gln Leu Ser Gly Gly Gln  
 470 475 480 485

caa caa cga gtc tct ata gcg aga gcc cta tta gga gtc cct cag tta 1603  
 Gln Gln Arg Val Ser Ile Ala Arg Ala Leu Leu Gly Val Pro Gln Leu  
 490 495 500

att att tgt gac gaa att gtt tct gct cta gat tta tct att caa gca 1651  
 Ile Ile Cys Asp Glu Ile Val Ser Ala Leu Asp Leu Ser Ile Gln Ala  
 505 510 515

caa att ctg aat atg ctt gcc gag ctg caa aaa aaa ctc agc ctc aca 1699  
 Gln Ile Leu Asn Met Leu Ala Glu Leu Gln Lys Lys Leu Ser Leu Thr  
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tat ctc ttc att tcg cat gat ctt gcc gtt gta cgc tcg ttc tgc aca 1747  
 Tyr Leu Phe Ile Ser His Asp Leu Ala Val Val Arg Ser Phe Cys Thr  
 535 540 545

gag gta ttc att atg tat aag ggg caa att gta gaa aaa gga aat aca 1795  
 Glu Val Phe Ile Met Tyr Lys Gly Gln Ile Val Glu Lys Gly Asn Thr  
 550 555 560 565

aaa cgc att ttt tct gat cca caa cat cct tat acg cgc atg ttg tta 1843  
 Lys Arg Ile Phe Ser Asp Pro Gln His Pro Tyr Thr Arg Met Leu Leu  
 570 575 580

aat gcc caa ctt cca gag act cct gat caa agg caa tct aaa cct ata 1891  
 Asn Ala Gln Leu Pro Glu Thr Pro Asp Gln Arg Gln Ser Lys Pro Ile  
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ttc caa gaa tat cac aaa gat tct gaa gaa tct tgc tct aca gga tgc 1939  
 Phe Gln Glu Tyr His Lys Asp Ser Glu Glu Ser Cys Ser Thr Gly Cys  
 600 605 610

tac ttt tac aat cgt tgt cca caa aaa caa gaa gct tgc aag tca gag 1987  
 Tyr Phe Tyr Asn Arg Cys Pro Gln Lys Gln Glu Ala Cys Lys Ser Glu  
 615 620 625

atc atc cca aat caa gga gac gcg cac cat aca tac cgt tgt atc cat 2035  
 Ile Ile Pro Asn Gln Gly Asp Ala His His Thr Tyr Arg Cys Ile His  
 630 635 640 645

tgattcgtcc tctacgctat tcttaagcta ccattaagga atcccaaggg agaggtctgc 2095  
 tctat 2100

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 <212> PRT  
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<220>  
 <221> SITE  
 <222> (59)..(67)

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<220>  
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 <222> (101)..(2194)

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20 acacgcttcg aagaaaaacg ttgcaagtcc ttcgacctct atg cca gga atc gag 115  
 Met Pro Gly Ile Glu  
 1 5

aaa gca gca aca aca gtg gct gta cct caa gac aaa tct gaa gaa gaa 163  
 Lys Ala Ala Thr Thr Val Ala Val Pro Gln Asp Lys Ser Glu Glu Glu  
 10 15 20

30 aaa gtt aaa gag cga ttg aca aag cgg gaa ctt acc tgt gaa gac ctt 211  
 Lys Val Lys Glu Arg Leu Thr Lys Arg Glu Leu Thr Cys Glu Asp Leu  
 25 30 35

aaa gat aac ggc tat act gtc aat ttt gaa gac att tct att tta gag 259  
 Lys Asp Asn Gly Tyr Thr Val Asn Phe Glu Asp Ile Ser Ile Leu Glu  
 40 45 50

ttg ttg cag ttc gta agt aaa att tct gga acg aac ttt gtc ttt gat 307  
 Leu Leu Gln Phe Val Ser Lys Ile Ser Gly Thr Asn Phe Val Phe Asp  
 55 60 65

40 agc aac gat ttg caa ttc aat gtc acg atc gtt tcc cac gat cct act 355  
 Ser Asn Asp Leu Gln Phe Asn Val Thr Ile Val Ser His Asp Pro Thr  
 70 75 80 85

tct gta gat gat tta tct aca atc tta cta caa gtc tta aaa atg cat 403  
 Ser Val Asp Asp Leu Ser Thr Ile Leu Leu Gln Val Leu Lys Met His  
 90 95 100

50 gac ttg aag gtt gtt gaa caa ggc aat aac gtc ctt atc tat cgt aat 451  
 Asp Leu Lys Val Val Glu Gln Gly Asn Asn Val Leu Ile Tyr Arg Asn  
 105 110 115

cct cat ctt tct aag cta tcc aca gta gtc aca gac agc tcc tta aaa 499  
 Pro His Leu Ser Lys Leu Ser Thr Val Val Thr Asp Ser Ser Leu Lys  
 120 125 130

gaa acg tgt gaa gct gtt gtg gtt acc cga gtg ttc cgt ctt tac agg 547  
 Glu Thr Cys Glu Ala Val Val Thr Arg Val Phe Arg Leu Tyr Arg  
 135 140 145

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	cgt cag ccc tct gca gca gta aat att att caa cct tta ctt tcc cat	595
	Arg Gln Pro Ser Ala Ala Val Asn Ile Ile Gln Pro Leu Leu Ser His	
	150 155 160 165	
	gat gct atc gtt agt gct tca gaa gct act cgt cat gtt atc atc tgc	643
	Asp Ala Ile Val Ser Ala Ser Glu Ala Thr Arg His Val Ile Ile Ser	
	170 175 180	
10	gat att gct ggt aat gtc gat aaa gtc agt gat ttg cta gca gct cta	691
	Asp Ile Ala Gly Asn Val Asp Lys Val Ser Asp Leu Leu Ala Ala Leu	
	185 190 195	
	gat tgc cca ggc aca tct gtg gac atg act gaa tac gaa gtt aaa tat	739
	Asp Cys Pro Gly Thr Ser Val Asp Met Thr Glu Tyr Glu Val Lys Tyr	
	200 205 210	
20	gcc aat ccc gca gct ctt gtt agc tac tgc caa gat gtt ctt ggt act	787
	Ala Asn Pro Ala Ala Leu Val Ser Tyr Cys Gln Asp Val Leu Gly Thr	
	215 220 225	
	ctg gcc gaa gat gat gct ttc caa atg ttc atc caa cct gga acg aac	835
	Leu Ala Glu Asp Asp Ala Phe Gln Met Phe Ile Gln Pro Gly Thr Asn	
	230 235 240 245	
	aaa att ttc gtc gtc tct tca cca cgt ctt gca aat aag gca gag cag	883
	Lys Ile Phe Val Val Ser Ser Pro Arg Leu Ala Asn Lys Ala Glu Gln	
	250 255 260	
30	ctc ctg aag tcc tta gat gtc cca gaa atg gca cat acc cta gat gat	931
	Leu Leu Lys Ser Leu Asp Val Pro Glu Met Ala His Thr Leu Asp Asp	
	265 270 275	
	cct gca agt act gcc ttg gct ttg gga gga aca gga acc acg agc cct	979
	Pro Ala Ser Thr Ala Leu Ala Leu Gly Gly Thr Gly Thr Thr Ser Pro	
	280 285 290	
40	aag agt ttg cgg ttc ttt atg tac aag ctg aag tat caa aat gga gaa	1027
	Lys Ser Leu Arg Phe Phe Met Tyr Lys Leu Lys Tyr Gln Asn Gly Glu	
	295 300 305	
	gtg att gct aat gcc ctc caa gat atc ggt tac aat cta tat gta acc	1075
	Val Ile Ala Asn Ala Leu Gln Asp Ile Gly Tyr Asn Leu Tyr Val Thr	
	310 315 320 325	
	aca gct atg gac gaa gat ttc att aac act ctc aat agt atc cag tgg	1123
	Thr Ala Met Asp Glu Asp Phe Ile Asn Thr Leu Asn Ser Ile Gln Trp	
	330 335 340	
50	tta gag gtc aat aac tcc ata gtt att atc gga aac caa ggg aat gtc	1171
	Leu Glu Val Asn Asn Ser Ile Val Ile Ile Gly Asn Gln Gly Asn Val	
	345 350 355	
	gac aga gtt att ggc ctc tta aac ggt tta gat tta cct cct aaa cag	1219
	Asp Arg Val Ile Gly Leu Leu Asn Gly Leu Asp Leu Pro Pro Lys Gln	
	360 365 370	
60	gtt tac atc gaa gtt tta att cta gat acc agc tta gag aaa tcc tgg	1267
	Val Tyr Ile Glu Val Leu Ile Leu Asp Thr Ser Leu Glu Lys Ser Trp	
	375 380 385	

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	gac ttt gga gtg caa tgg gta gcc cta ggt gat gaa caa agt aaa gta	1315
	Asp Phe Gly Val Gln Trp Val Ala Leu Gly Asp Glu Gln Ser Lys Val	
	390 395 400 405	
	gct tat gct tct gga cta ttg aat aat act ggc ata gcc aca cct aca	1363
	Ala Tyr Ala Ser Gly Leu Leu Asn Asn Thr Gly Ile Ala Thr	
	410 415 420	
10	aaa gca act gtc cct ccc ggc acg cca aat cct ggt tcg atc cct ctt	1411
	Lys Ala Thr Val Pro Pro Gly Thr Pro Asn Pro Gly Ser Ile Pro Leu	
	425 430 435	
	cct acg cca gga caa ttg aca ggg ttc tca gat atg ctg aac tct tcg	1459
	Pro Thr 440 Pro Gly Gln Leu Thr 445 Phe Ser Asp Met Leu Asn Ser Ser	
	445 450	
20	tca gca ttc ggt cta gga atc atc gga aat gtc cta agt cat aaa ggg	1507
	Ser Ala Phe Gly Leu Gly Ile Ile Gly Asn Val Leu Ser His Lys Gly	
	455 460 465	
	aag tct ttc ctt act ttg gga ggc tta tta agt gcc tta gat caa gat	1555
	Lys Ser Phe Leu Thr Leu Gly Gly Leu Leu Ser Ala Leu Asp Gln Asp	
	470 475 480 485	
	gga gat act gtc att gtc ttg aat cct aga atc atg gct cag gat acg	1603
	Gly Asp Thr Val Ile Val Leu Asn Pro Arg Ile Met Ala Gln Asp Thr	
	490 495 500	
30	caa caa gct tcg ttt ttt gta ggg caa acg gtc cct tac caa act atc	1651
	Gln Gln Ala Ser Phe Phe Val Gly Gln Thr Val Pro Tyr Gln Thr Ile	
	505 510 515	
	aaa tac tat atc caa gaa aca gga act gta acg caa aat atc gat tat	1699
	Lys Tyr Tyr Ile Gln Glu Thr Gly Thr Val Thr Gln Asn Ile Asp Tyr	
	520 525 530	
40	gaa gat att gga gtg aac ctt gtc gtt acc tct aca gtt gct ccc aac	1747
	Glu Asp Ile Gly Val Asn Leu Val Val Thr Ser Thr Val Ala Pro Asn	
	535 540 545	
	aat gta gtt aca cta caa atc gaa cag acg atc tca gaa tta cat tcc	1795
	Asn Val Val Thr Leu Gln Ile Glu Gln Thr Ile Ser Glu Leu His Ser	
	550 555 560 565	
	gcg tct gga tca cta aca cct gtc aca gat aaa act tat gca gcc aca	1843
	Ala Ser Gly Ser Leu Thr Pro Val Thr Asp Lys Thr Tyr Ala Ala Thr	
	570 575 580	
50	cgc tta caa att ccc gac ggt tgt ttc tta gtt atg agt ggg cat atc	1891
	Arg Leu Gln Ile Pro Asp Gly Cys Phe Leu Val Met Ser Gly His Ile	
	585 590 595	
	aga gat aaa act aca aaa gtg gtt tca gga gtg cct ttg cta aac tcc	1939
	Arg Asp Lys Thr Thr Lys Val Val Ser Gly Val Pro Leu Leu Asn Ser	
	600 605 610	
60	ata cca tta att cgt ggt tta ttt agc cgt acc atc gac caa agg caa	1987
	Ile Pro Leu Ile Arg Gly Leu Phe Ser Arg Thr Ile Asp Gln Arg Gln	
	615 620 625	



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aaa cgc aat atc atg atg ttt att aag cct aag gtg att agt agc ttt 2035
Lys Arg Asn Ile Met Met Phe Ile Lys Pro Lys Val Ile Ser Ser Phe
630 635 640 645

gaa gaa ggc act cgt gtt acc aat aag gaa gga tac aga tac aat tgg 2083
Glu Glu Gly Thr Arg Val Thr Asn Lys Glu Gly Tyr Arg Tyr Asn Trp
650 655 660

gaa gct gat gaa gga tcc atg caa gtg gcc cct cgc cat gct cct gaa 2131
Glu Ala Asp Glu Gly Ser Met Gln Val Ala Pro Arg His Ala Pro Glu
665 670 675

tgc caa gga cct cct tct tta cag gct gaa agt gac ttt aaa ata ata 2179
Cys Gln Gly Pro Pro Ser Leu Gln Ala Glu Ser Asp Phe Lys Ile Ile
680 685 690

gaa ata gaa gct cag tagtggtata taaaagagga agatgatatt ctccgccgtg 2234
Glu Ile Glu Glu Ala Gln
695

gaatagcttc tgactctggt gcattcaggg gaaaagccaa gaagatgtag agtcggccgt 2294
ataact 2300

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<222> (50)..(58)

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<213> Chlamydia pneumoniae

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Met Ser Arg Lys Asp
1 5

aat gag gtt tcc tta gct cgt tca att ttt aat ata tta tcc gga act 163
Asn Glu Val Ser Leu Ala Arg Ser Ile Phe Asn Ile Leu Ser Gly Thr
10 15 20

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60

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	ttc tgt agt cgt att aca ggg ata ttt cga gaa att gca atg gca acc	211
	Phe Cys Ser Arg Ile Thr Gly Ile Phe Arg Glu Ile Ala Met Ala Thr	
	25 30 35	
	tat ttt gga gct gat cca att gta gct gct ttc tgg tta ggt ttc cgt	259
	Tyr Phe Gly Ala Asp Pro Ile Val Ala Ala Phe Trp Leu Gly Phe Arg	
	40 45 50	
10	act gtt ttt ttc tta aga aaa att tta gga ggg ctc att cta gaa caa	307
	Thr Val Phe Phe Leu Arg Lys Ile Leu Gly Gly Leu Ile Leu Glu Gln	
	55 60 65	
	gcc ttc atc cct cat ttt gaa ttt ctc cgt gct caa agt ctc gat cgt	355
	Ala Phe Ile Pro His Phe Glu Phe Leu Arg Ala Gln Ser Leu Asp Arg	
	70 75 80 85	
20	gcg gcg ttt ttt ttc cga cgc ttt tct aga ttg att aaa gcc agc act	403
	Ala Ala Phe Phe Phe Arg Arg Phe Ser Arg Leu Ile Lys Gly Ser Thr	
	90 95 100	
	att ata ttc act ctg ctt att gaa gca gta ttg tgg gta ttc ttc aat	451
	Ile Ile Phe Thr Leu Leu Ile Glu Ala Val Leu Trp Val Phe Phe Asn	
	105 110 115	
	aac gtt gaa gag ggg act tac gat atg att ctc ctt act atg ata ctc	499
	Asn Val Glu Glu Gly Thr Tyr Asp Met Ile Leu Leu Thr Met Ile Leu	
	120 125 130	
30	ttg ccc tgt ggc att ttc tta atg atg tac aat gta aac gcc gct ttg	547
	Leu Pro Cys Gly Ile Phe Leu Met Met Tyr Asn Val Asn Gly Ala Leu	
	135 140 145	
	ctt cac tgt gga aat aag ttt ttc ggg gtg gga tta gct ccc gta gtt	595
	Leu His Cys Gly Asn Lys Phe Phe Gly Val Gly Leu Ala Pro Val Val	
	150 155 160 165	
40	gta aat atc att tgg att ttc ttt gtt ata gcg gct cgt cat tca gat	643
	Val Asn Ile Ile Trp Ile Phe Phe Val Ile Ala Ala Arg His Ser Asp	
	170 175 180	
	cct aga gag cgt att atc ggt tta tcc gtg gct cta gtt atc ggg ttt	691
	Pro Arg Glu Arg Ile Ile Gly Leu Ser Val Ala Leu Val Ile Gly Phe	
	185 190 195	
	ttc ttc gaa tgg tta atc acg gtt cct gga gta tgg aaa ttt cta tta	739
	Phe Phe Glu Trp Leu Ile Thr Val Pro Gly Val Trp Lys Phe Leu Leu	
	200 205 210	
50	gaa gcg aag agc cca cct caa gaa cac gat agt gtt cga gct tta tta	787
	Glu Ala Lys Ser Pro Pro Gln Glu His Asp Ser Val Arg Ala Leu Leu	
	215 220 225	
	gct ccc tta tct ttg ggt att tta act tca agc atc ttc cag ctg aac	835
	Ala Pro Leu Ser Leu Gly Ile Leu Thr Ser Ser Ile Phe Gln Leu Asn	
	230 235 240 245	
60	ctt ctt tct gat atc tgc ttg gct cgc tat gta cat gaa ata ggc cct	883
	Leu Leu Ser Asp Ile Cys Leu Ala Arg Tyr Val His Glu Ile Gly Pro	
	250 255 260	

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	cta tat ctt atg tac tcc tta aag att tat cag ctc ccc ata cat ctc	931
	Leu Tyr Leu Met Tyr Ser Leu Lys Ile Tyr Gln Leu Pro Ile His Leu	
	265 270 275	
	ttt ggc ttt ggt gtg ttt acc gtt ctc ctc cca gca att tct cgt tgt	979
	Phe Gly Phe Gly Val Phe Thr Val Leu Leu Pro Ala Ile Ser Arg Cys	
	280 285 290	
10	gta cag cga gaa gat cat gag agg gga ttg aaa ctt atg aag ttc gtt	1027
	Val Gln Arg Glu Asp His Glu Arg Gly Leu Lys Met Lys Phe Val	
	295 300 305	
	ctc acc cta acc atg tcc gta atg atc att atg aca gca ggg cta ttg	1075
	Leu Thr Leu Thr Met Ser Val Met Ile Ile Met Thr Ala Gly Leu Leu	
	310 315 320 325	
20	ctc tta gct tta cct gga gtc cgt gtc ctt tat gaa cac gga ctt ttc	1123
	Leu Leu Ala Leu Pro Gly Val Arg Val Leu Tyr Glu His Gly Leu Phe	
	330 335 340	
	cct cag agt gct gtc tac gct att gtt cgt gta ttg cga ggt tat ggt	1171
	Pro Gln Ser Ala Val Tyr Ala Ile Val Arg Val Leu Arg Gly Tyr Gly	
	345 350 355	
	gcc agt att atc cct atg gcc ttg gct cct tta gtc tct gtt ctt ttt	1219
	Ala Ser Ile Ile Pro Met Ala Leu Ala Pro Leu Val Ser Val Leu Phe	
	360 365 370	
30	tat gca cag cgg cag tat gct gtt ccg ctc ttt ata gga atc ggt acg	1267
	Tyr Ala Gln Arg Gln Tyr Ala Val Pro Leu Phe Ile Gly Ile Gly Thr	
	375 380 385	
	gct ttg gcc aat att gtt tta agc ttg gtt cta ggt cgt tgg gtt tta	1315
	Ala Leu Ala Asn Ile Val Leu Ser Leu Val Leu Gly Arg Trp Val Leu	
	390 395 400 405	
40	aaa gac gtc tcg ggc att tcc tat gct aca tcc ata act gct tgg gtg	1363
	Lys Asp Val Ser Gly Ile Ser Tyr Ala Thr Ser Ile Thr Ala Trp Val	
	410 415 420	
	cag tta tat ttc ctc tgg tat tat tct tcg aaa aga ctc cct atg tac	1411
	Gln Leu Tyr Phe Leu Trp Tyr Tyr Ser Lys Arg Leu Pro Met Tyr	
	425 430 435	
	tct aag tta ctt tgg gag agc atc cgg cgt tcc ata aaa gtt atg gga	1459
	Ser Lys Leu Leu Trp Glu Ser Ile Arg Arg Ser Ile Lys Val Met Gly	
	440 445 450	
50	acc act atg ctt gct tgt atg att act cta ggc tta aat atc ctt acg	1507
	Thr Thr Met Leu Ala Cys Met Ile Thr Leu Gly Leu Asn Ile Leu Thr	
	455 460 465	
	caa act aca tat gta att ttc tta aac ccc ctc aca cca ctt gct tgg	1555
	Gln Thr Thr Tyr Val Ile Phe Leu Asn Pro Leu Thr Pro Leu Ala Trp	
	470 475 480 485	
60	ccc tta tcc tcc ata acg gct caa gca att gct ttt tta tct gag agc	1603
	Pro Leu Ser Ser Ile Thr Ala Gln Ala Ile Ala Phe Leu Ser Glu Ser	
	490 495 500	

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tgc att ttc ttg gct ttt ttg ttt ggt ttt gca aaa ctg ctt cga gta 1651
Cys Ile Phe Leu Ala Phe Leu Phe Gly Phe Ala Lys Leu Leu Arg Val
                    505                    510                    515

gaa gat ctt att aat ttg gct tct ttt gaa tac tgg cgt ggg caa cgg 1699
Glu Asp Leu Ile Asn Leu Ala Ser Phe Glu Tyr Trp Arg Gly Gln Arg
                    520                    525                    530

ggt ctt ttg caa aga caa cac gtg atg caa gac act caa aat 1741
Gly Leu Leu Gln Arg Gln His Val Met Gln Asp Thr Gln Asn
                    535                    540                    545

taatcatgtt tgtttcttgt agctcagtcg ctttctttta gctttaagtt ttgatagcct 1801
gcttggtcct ctgtttctac acttaatat gatactaagg atactatgaa aaaacaggta 1861
tatcaatggt tagcgagtgt ggttctttta gcgctgaca 1900

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    <213> Chlamydia pneumoniae

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    <221> SITE
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                    Met Lys Thr Ser Arg
                              1                    5

50 aat aaa cag tgc aaa ata aca gat ccc tta agt aaa tct tcc ttc ttt 163
    Asn Lys Gln Cys Lys Ile Thr Asp Pro Leu Ser Lys Ser Ser Phe Phe
                              10                    15                    20

    gtt gga gcc tta att tta ggt aaa act aca ata ctc ctt aat gcg act 211
    Val Gly Ala Leu Ile Leu Gly Lys Thr Thr Ile Leu Leu Asn Ala Thr
                              25                    30                    35

    ccg ttg tct gac tat ttt gat aat caa gca aat caa ctc aca aca ctc 259
    Pro Leu Ser Asp Tyr Phe Asp Asn Gln Ala Asn Gln Leu Thr Thr Leu
                              40                    45                    50

60
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	gca aca ctt ttt gga gtt agg gat gac act aac caa gac att gtc ctc	355
	Ala Thr Leu Phe Gly Val Arg Asp Asp Thr Asn Gln Asp Ile Val Leu	
	70 75 80 85	
10	gat cac cag aat tcc ata gaa agc tgg ttc gaa aac ttc tct caa gac	403
	Asp His Gln Asn Ser Ile Glu Ser Trp Phe Glu Asn Phe Ser Gln Asp	
	90 95 100	
	ggc ggt gct ctc tct tgc aaa tca ctt gcc ata acg aat aca aaa aac	451
	Gly Gly Ala Leu Ser Cys Lys Ser Leu Ala Ile Thr Asn Thr Lys Asn	
	105 110 115	
20	caa att ctt ttc cta aat agc ttt gct att aaa aga gct ggt gcg atg	499
	Gln Ile Leu Phe Leu Asn Ser Phe Ala Ile Lys Arg Ala Gly Ala Met	
	120 125 130	
	tat gtt gat ggt aat ttc gat ctt tct gag aat cat ggt tcc atc att	547
	Tyr Val Asp Gly Asn Phe Asp Leu Ser Glu Asn His Gly Ser Ile Ile	
	135 140 145	
	ttc tct ggg aat tta agc ttt cct aat gca agt aat ttc gct gat act	595
	Phe Ser Gly Asn Leu Ser Phe Pro Asn Ala Ser Asn Phe Ala Asp Thr	
	150 155 160 165	
30	tgt aca ggg gga gct gtt tta tgt tcg aaa aat gtt aca atc tca aaa	643
	Cys Thr Gly Gly Ala Val Leu Cys Ser Lys Asn Val Thr Ile Ser Lys	
	170 175 180	
	aat caa gga acc gca tac ttc att aac aac aag gca aaa tct tca gga	691
	Asn Gln Gly Thr Ala Tyr Phe Ile Asn Asn Lys Ala Lys Ser Ser Gly	
	185 190 195	
40	gga gca atc caa gct gca atc ata aac att aag gac aac act ggc cct	739
	Gly Ala Ile Gln Ala Ala Ile Ile Asn Ile Lys Asp Asn Thr Gly Pro	
	200 205 210	
	tgc ctg ttt ttt aat aat gct gca ggc gga aca gcg ggg ggc gcg ttg	787
	Cys Leu Phe Phe Asn Asn Ala Ala Gly Gly Thr Ala Gly Gly Ala Leu	
	215 220 225	
	ttc gct aat gct tgt aga att gag aat aat tct cag cct atc tat ttt	835
	Phe Ala Asn Ala Cys Arg Ile Glu Asn Asn Ser Gln Pro Ile Tyr Phe	
	230 235 240 245	
50	ttg aat aac caa tca ggt ctg ggt ggt gca ata aga gta cat caa gag	883
	Leu Asn Asn Gln Ser Gly Leu Gly Gly Ala Ile Arg Val His Gln Glu	
	250 255 260	
	tgc att ctt aca aag aat acc ggt tct gtg atc ttc aac aat aat ttt	931
	Cys Ile Leu Thr Lys Asn Thr Gly Ser Val Ile Phe Asn Asn Asn Phe	
	265 270 275	
60	gcc atg gaa gcg gac atc tct gct aac cat tcc tct gga ggg gct atc	979
	Ala Met Glu Ala Asp Ile Ser Ala Asn His Ser Ser Gly Gly Ala Ile	
	280 285 290	

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	tat tgc att agt tgt tct ata aaa gac aac cca gga att gca gcc ttc	1027
	Tyr Cys Ile Ser Cys Ser Ile Lys Asp Asn Pro Gly Ile Ala Ala Phe	
	295 300 305	
	gat aat aat act gca gca cga gat gga ggt gct atc tgt aca caa tct	1075
	Asp Asn Asn Thr Ala Arg Asp Gly Gly Ala Ile Cys Thr Gln Ser	
	310 315 320 325	
10	cta act ata caa gac agt ggt ccc gtc tat ttc aca aac aat cag gga	1123
	Leu Thr Ile Gln Asp Ser Gly Pro Val Tyr Phe Thr Asn Asn Gln Gly	
	330 335 340	
	act tgg ggc ggc gct atc atg ctc cgt caa gat ggt gca tgc act tta	1171
	Thr Trp Gly Gly Ala Ile Met Leu Arg Gln Asp Gly Ala Cys Thr Leu	
	345 350 355	
20	ttt gct gat cag gga gat att att ttt tat aat aat aga cac ttc aaa	1219
	Phe Ala Asp Gln Gly Asp Ile Ile Phe Tyr Asn Asn Arg His Phe Lys	
	360 365 370	
	gat act ttc agc aat cat gtt tct gta aac tgc acg cgt aat gtc tca	1267
	Asp Thr Phe Ser Asn His Val Ser Val Asn Cys Thr Arg Asn Val Ser	
	375 380 385	
	tta aca gtt gga gca agt caa ggt cat tct gct acc ttc tat gat ccc	1315
	Leu Thr Val Gly Ala Ser Gln Gly His Ser Ala Thr Phe Tyr Asp Pro	
	390 395 400 405	
30	ata cta caa aga tat act ata caa aac tct atc caa aaa ttt aat cct	1363
	Ile Leu Gln Arg Tyr Thr Ile Gln Asn Ser Ile Gln Lys Phe Asn Pro	
	410 415 420	
	aat cca gaa cac ctc gga act atc ttg ttc tcc tca aca tat att ccg	1411
	Asn Pro Glu His Leu Gly Thr Ile Leu Phe Ser Ser Thr Tyr Ile Pro	
	425 430 435	
40	gat aca tcg act tct cgt gat gac ttc att tca cat ttc aga aac cac	1459
	Asp Thr Ser Thr Ser Arg Asp Asp Phe Ile Ser His Phe Arg Asn His	
	440 445 450	
	att gga ctg tac aac ggc aca ctc gct ctt gaa gat cga gca gag tgg	1507
	Ile Gly Leu Tyr Asn Gly Thr Leu Ala Leu Glu Asp Arg Ala Glu Trp	
	455 460 465	
	aaa gtc tat aaa ttt gat caa ttt ggt ggg act cta cgg tta ggc agt	1555
	Lys Val Tyr Lys Phe Asp Gln Phe Gly Gly Thr Leu Arg Leu Gly Ser	
	470 475 480 485	
50	aga gct gtg ttt tct aca aca gac gaa gaa caa agt agc agt agt gtg	1603
	Arg Ala Val Phe Ser Thr Thr Asp Glu Glu Gln Ser Ser Ser Ser Val	
	490 495 500	
	ggt tct gta att aac atc aat aat ctt gca att aac ctt ccc tct atc	1651
	Gly Ser Val Ile Asn Ile Asn Asn Leu Ala Ile Asn Leu Pro Ser Ile	
	505 510 515	
60	tta ggc aac aga gtt gct ccc aag cta tgg att cgc ccc aca ggt tca	1699
	Leu Gly Asn Arg Val Ala Pro Lys Leu Trp Ile Arg Pro Thr Gly Ser	
	520 525 530	

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	tca gca ccc tat agc gaa gat aat aac cct ata atc aat ctc tca gga	1747
	Ser Ala Pro Tyr Ser Glu Asp Asn Asn Pro Ile Ile Asn Leu Ser Gly	
	535 540 545	
	cct ttg agc cta ctg gat gac gag aac cta gat ccc tat gat act gca	1795
	Pro Leu Ser Leu Leu Asp Asp Glu Asn Leu Asp Pro Tyr Asp Thr Ala	
	550 555 560 565	
10	gac ctt gcc caa cct atc gca gaa gtt cct ctt ctg tat ctc tta gac	1843
	Asp Leu Ala Gln Pro Ile Ala Glu Val Pro Leu Leu Tyr Leu Leu Asp	
	570 575 580	
	gtc aca gct aaa cat att aat acg gat aat ttc tac cct gag ggt cta	1891
	Val Thr Ala Lys His Ile Asn Thr Asp Asn Phe Tyr Pro Glu Leu Leu	
	585 590 595	
20	aat aca act caa cac tac gcc tac caa gcc gtt tgg tcc cct tac tgg	1939
	Asn Thr Thr Gln His Tyr Gly Tyr Gln Gly Val Trp Ser Pro Tyr Trp	
	600 605 610	
	atc gaa aca atc aca act tct gat acc tct tct gaa gat act gtg aat	1987
	Ile Glu Thr Ile Thr Thr Ser Asp Thr Ser Ser Glu Asp Thr Val Asn	
	615 620 625	
	act tta cat cgc cag ctt tat ggt gat tgg aca cct aca gga tat aag	2035
	Thr Leu His Arg Gln Leu Tyr Gly Asp Trp Thr Pro Thr Gly Tyr Lys	
	630 635 640 645	
30	gta aac cca gaa aac aaa gga gac att gcc cta tct gcc ttc tgg caa	2083
	Val Asn Pro Glu Asn Lys Gly Asp Ile Ala Leu Ser Ala Phe Trp Gln	
	650 655 660	
	tct ttc cat aac tta ttt gcg aca cta cgt tat caa aca cag caa gcc	2131
	Ser Phe His Asn Leu Phe Ala Thr Leu Arg Tyr Gln Thr Gln Gly	
	665 670 675	
40	caa ata gca cct aca gct tct gga gaa gct act cga ctc ttc gtg cat	2179
	Gln Ile Ala Pro Thr Ala Ser Gly Glu Ala Thr Arg Leu Phe Val His	
	680 685 690	
	caa aat agc aac aat gat gcg aaa gga ttc cat atg gaa gct acg ggt	2227
	Gln Asn Ser Asn Asn Asp Ala Lys Gly Phe His Met Glu Ala Thr Gly	
	695 700 705	
	tat tct ttg gga aca acc tca aac act gct tct aat cat agc ttt ggt	2275
	Tyr Ser Leu Gly Thr Thr Ser Asn Thr Ala Ser Asn His Ser Phe Gly	
	710 715 720 725	
50	gta aac ttc tcc caa ctt ttc agt aat ctc tac gag agc cac tcc gac	2323
	Val Asn Phe Ser Gln Leu Phe Ser Asn Leu Tyr Glu Ser His Ser Asp	
	730 735 740	
	aat tcc gtg gct tcg cat acg aca act gta gcg ctc cag atc aat aat	2371
	Asn Ser Val Ala Ser His Thr Thr Thr Val Ala Leu Gln Ile Asn Asn	
	745 750 755	
60	cct tgg ctg caa gag aga ttc tct aca tct gca tct cta gcc tac agc	2419
	Pro Trp Leu Gln Glu Arg Phe Ser Thr Ser Ala Ser Leu Ala Tyr Ser	
	760 765 770	

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tac agc aac cac cat atc aaa gca tct gga tat tct gga aaa ata caa 2467  
 Tyr Ser Asn His His Ile Lys Ala Ser Gly Tyr Ser Gly Lys Ile Gln  
 775 780 785

acg gaa ggc aaa tgt tat agt acg aca tta ggg gcg gct ctc tct tgc 2515  
 Thr Glu Gly Lys Cys Tyr Ser Thr Thr Leu Gly Ala Ala Leu Ser Cys  
 790 795 800 805

10 tct cta tct cta caa tgg cga tca cga cct ctc cac ttc act cct ttt 2563  
 Ser Leu Ser Ser Leu Trp Arg Ser Arg Pro Leu His Phe Thr Pro Phe  
 810 815 820

atc caa gca att gcc gtt cgt tct aat caa act gcg ttt caa gaa agt 2611  
 Ile Gln Ala Ile Ala Val Arg Ser Asn Gln Thr Ala Phe Gln Ser  
 825 830 835

20 gga gat aaa gct aga aaa ttt tct gtt cat aaa ccc tta tat aac ctg 2659  
 Gly Asp Lys Ala Arg Lys Phe Ser Val His Lys Pro Leu Tyr Asn Leu  
 840 845 850

aca gtc cct ctg gga att cag agc gct tgg gaa tcc aag ttc cgt ctt 2707  
 Thr Val Pro Leu Gly Ile Gln Ser Ala Trp Glu Ser Lys Phe Arg Leu  
 855 860 865

cct acc tat tgg aac ata gag ctt gct tat cag cct gtc ctc tac caa 2755  
 Pro Thr Tyr Trp Asn Ile Glu Leu Ala Tyr Gln Pro Val Leu Tyr Gln  
 870 875 880 885

30 caa aat cct gag atc aac gtg agt cta gaa tct agt gga tcg tca tgg 2803  
 Gln Asn Pro Glu Ile Asn Val Ser Leu Glu Ser Ser Gly Ser Ser Trp  
 890 895 900

ctc cta tca gga acc acc ctt gct cgc aat gcc att gct ttt aaa gga 2851  
 Leu Leu Ser Gly Thr Thr Leu Ala Arg Asn Ala Ile Ala Phe Lys Gly  
 905 910 915

40 aga aac caa att ttt atc ttc cct aaa ctt tcg gtg ttc tta gac tat 2899  
 Arg Asn Gln Ile Phe Ile Phe Pro Lys Leu Ser Val Phe Leu Asp Tyr  
 920 925 930

caa ggc tcg gta tcc tca tca acg acg aca cat tac ctt cac gca gga 2947  
 Gln Gly Ser Val Ser Ser Ser Thr Thr Thr His Tyr Leu His Ala Gly  
 935 940 945

acg acc ttt aag ttt taaaagcatg ttatatagac aatgcaacct gtaagacca 3002  
 Thr Thr Phe Lys Phe  
 950

50 aatagagagt agtgaacct ctctaccatc atgaatctta tgggagaagc taagggaat 3062  
 ccacagatac gtttccccc taaaaattaa gaaccgcgata catcctcact agagattcga 3122  
 aagaactact taaatcctaa gcattcga 3150

<210> 20  
 <211> 9  
 <212> PRT  
 <213> Chlamydia pneumoniae

60 <220>



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<221> SITE  
 <222> (119)..(127)

<400> 20  
 Ile Leu Phe Leu Asn Ser Phe Ala Ile  
 1 5

10

<210> 21  
 <211> 3200  
 <212> DNA  
 <213> Chlamydia pneumoniae

<220>  
 <221> CDS  
 <222> (101)..(3100)

20

<400> 21  
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 cactctctccc ttgattactact ctgcggatat ttcttctctcc acgctgagatc actacttaaa 180  
 cgtggcgagtg agaattgagat ttttaacaat aagtgaccaa aacagaaaaga ttaagggaacc 240  
 tctagtgtca aagactcctc ctaagttttt attctatctc gggaatttca cagcctgcat 300  
 gttcgggatg actcctgcag tgatagtttt acaaacggac tcccttgaata agtttggcttt 360  
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 aggatcttct ccaataacta cgtttgttgg aaatagacat aattctctctc aagacattgt 480  
 actttctaac tacaagtcta ttgataacat ccttctcttt tggacatcgg ctggggggagc 540  
 tctgtctctgt aataatttct tattatcaaa tgttgaagac catgctctct tcagtataaaa 600  
 tctgcgattt gggactggag gcgcgattgc ttgccaggga gctgcacaaa tcacgaagaa 660  
 tagaggacccc ctattttttt tcagcaatcg aggtcttaac aatgcgagta caggaggaga 720  
 aactcgtggg ggtgcgattg cctgtaattg agacttcacg atttctcaaa atcaaggagac 780  
 tttctacttt gtcaacaatt cgtcaacaaa ctggggagga gccctctcca ccaatggaca 840  
 ctgcccgcac caaagcaaca gggcacctct actctttttt aacaatacag cccctagtgg 900  
 agggggtgcg ctctgtagtg aaaatacaac gatctctgat aacacgcgtc ctattttatt 960  
 taagaacaac tgtgggaaga atggcggggc cattcaaaac agcgttactg ttgcgataaa 1020  
 aaataactccc gggctgttga tttcaataaa caacacagcg tatctgtgtt cgataaaatc 1080  
 aggaataggt tcaggagggg cgatttatatc aacaaaccta tccatagacg ataacctctg 1140  
 aactactctt ttcaataata actactgcac tgcgcatctc gtagcatctc gtacacaatt 1200  
 40 tttgacaactc aaaaatagtg gccacgtata ttccaccac aatcaaggaa actggggagg 1260  
 tgtctctatg ctctcacagg acagcacctg cctactcttc gcggaacaaag gaaatatcgc 1320  
 atttcaaaat aatgaggttt tctctaccac atttggtaga tacaacgcga tacattgtac 1380  
 accaaatagc aacttaaac ttggagctaa taagggtgat acgactgctt ttttgatccc 1440  
 tatagaacac caacatccaa ctacaaatcc tctaatcttt aatcccaatg cgaaccatca 1500  
 gggaacgatc ttattttctt cagcctatat cccagaagct tctgactacg aaaaatttt 1560  
 cattagcagc tcgaaaaata cctctgaact tcgcaattgt gtctctctta tgcaggatcg 1620  
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 50 catcattaat aaccttcgca ttaacctccc ctcgatctta gcaaaaggaa aagctcctac 1800  
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 tactttatca ggtcctctga cactcttaaa tgaggaaaac cgcgactccc acgacagbat 1920  
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 tctagaattt caggggatg ccgacggcct ctttgttcat caaaatagca tcccggggg 2340  
 60 cccagatcgc cgattccaat ctacagggta tctcttcaaa cactctccc aaactctttt 2400  
 acatcagaaa atctccttag gttttgcaca gttcttcacc cgcactaaaag aaactcggtac 2460

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```

aagcaacaac gtctcggtc acaatacagt ctcttcactt tatgttgagc ttccgtggtt 2520
ccaagaggcc ttgtcaacat cccacagttt agcgtatggc tatggggacc atcacctcca 2580
cgctcatatc cgtcacatca agaacagggc agaaggagc tggtatagcc atacattagc 2640
agcagctatc ggctgttctt tcccttggca acagaaatcc tatcttcacc tcagcccggt 2700
cggtcaggga attgcaatac gttctcacca aacagcgttc gaagagattg gtgacaatcc 2760
cogaaagtgt gtctctcaaa agcctttcta taatctgacc ttacctctag gaatccaagg 2820
10  aaaaatggcag tcaaaaatcc acgtacctac agaattggact ctagaacttt cttaccaacc 2880
    ggtactctat caacaaaatc cccaaatcgg tgtcacgcta ctctcgagcg gaggttcctg 2940
    ggatatccta ggccataact atgttcgcaa tgctttaggg tacaaagtcc acaatcaaac 3000
    tgcgtctctc cgttctctcg atctattctt ggattaccaa ggatcggtct cctcctcgac 3060
    atctacgcac catctccaag caggaagtac cttaaaatcc taaaaataaa gaacgataaa 3120
    attgaaatct ttagaattaa caactatccg atgagctacg ttagcccaat cggtagagga 3180
    ctccctcaaa atttaataaa 3200

```

```

<210> 22
<211> 9
20 <212> PRT
    <213> Chlamydia pneumoniae

```

```

<220>
<221> SITE
<222> (56) .. (64)

```

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<400> 22
Phe Leu Phe Tyr Leu Gly Asn Phe Thr
1           5

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```

30 <210> 23
    <211> 3000
    <212> DNA
    <213> Chlamydia pneumoniae

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<220>
<221> CDS
40 <222> (101) .. (2893)

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<400> 23
tagacactat aaaacaaatt atagacaaaa aatctagcat tgatttatcc agaattatcc 60

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```

tttctatttg tgaacgagta tgcgcttttt ttgcttcgga atg ttg ctt cct ttt 115
                Met Leu Leu Pro Phe
                1           5

```

```

act ttt gta ttg gct aat gaa ggt ctc caa ctt cct ttg gag acc tat 163
Thr Phe Val Leu Ala Asn Glu Gly Leu Gln Leu Pro Leu Glu Thr Tyr
                10           15           20

```

```

att aca tta agt cct gaa tat caa gca gcc cct caa gta ggg ttt act 211
Ile Thr Leu Ser Pro Glu Tyr Gln Ala Ala Pro Gln Val Gly Phe Thr
                25           30           35

```

```

cat aac caa aat caa gat ctc gca att gtc ggg aat cac aat gat ttc 259
His Asn Gln Asn Gln Asp Leu Ala Ile Val Gly Asn His Asn Asp Phe
                40           45           50

```

60

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	atc	ttg	gac	tat	aag	tac	tat	cgg	tcg	aat	gga	ggg	gct	ctt	acc	tgt	307
	Ile	Leu	Asp	Tyr	Lys	Tyr	Tyr	Arg	Ser	Asn	Gly	Gly	Ala	Leu	Thr	Cys	
		55					60					65					
	aag	aat	ctt	ctg	atc	tct	gaa	aat	ata	ggg	aat	gtc	ttc	ttt	gag	aag	355
	Lys	Asn	Leu	Leu	Ile	Ser	Glu	Asn	Ile	Gly	Asn	Val	Phe	Phe	Glu	Lys	
		70				75					80					85	
10	aat	gtc	tgt	ccc	aat	tct	ggc	ggg	gca	att	tat	gct	gct	caa	aat	tgc	403
	Asn	Val	Cys	Pro	Lys	Ser	Gly	Gly	Ala	Ile	Tyr	Ala	Ala	Gln	Asn	Cys	
					90					95					100		
	acg	atc	tcc	aag	aat	cag	aac	tat	gca	ttt	act	aca	aac	ttg	gtc	tct	451
	Thr	Ile	Ser	Lys	Asn	Gln	Asn	Tyr	Ala	Phe	Thr	Thr	Asn	Leu	Val	Ser	
				105					110					115			
20	gac	aat	cct	aca	gcc	act	gcg	gga	tca	cta	ttg	ggg	gga	gct	ctc	ttt	499
	Asp	Asn	Pro	Thr	Ala	Thr	Ala	Gly	Ser	Leu	Leu	Gly	Gly	Ala	Leu	Phe	
			120					125					130				
	gcc	ata	aat	tgc	tct	att	act	aat	aac	cta	gga	cag	gga	act	ttc	gtt	547
	Ala	Ile	Asn	Cys	Ser	Ile	Thr	Asn	Asn	Leu	Gly	Gln	Gly	Thr	Phe	Val	
		135					140					145					
	gac	aat	ctc	gct	tta	aat	aag	ggg	ggg	gcc	ctc	tat	act	gag	acg	aac	595
	Asp	Asn	Leu	Ala	Leu	Asn	Lys	Gly	Gly	Ala	Leu	Tyr	Thr	Glu	Thr	Asn	
		150				155					160					165	
30	tta	tct	att	aaa	gac	aat	aaa	ggc	ccg	atc	ata	atc	aag	cag	aat	cgg	643
	Leu	Ser	Ile	Lys	Asp	Asn	Lys	Gly	Pro	Ile	Ile	Ile	Lys	Gln	Asn	Arg	
					170					175					180		
	gca	cta	aat	tcg	gac	agt	tta	gga	gga	ggg	att	tat	agt	ggg	aac	tct	691
	Ala	Leu	Asn	Ser	Asp	Ser	Leu	Gly	Gly	Gly	Ile	Tyr	Ser	Gly	Asn	Ser	
				185					190					195			
40	cta	aat	ata	gag	gga	aat	tct	gga	gct	ata	cag	atc	aca	agc	aac	tct	739
	Leu	Asn	Ile	Glu	Gly	Asn	Ser	Gly	Ala	Ile	Gln	Ile	Thr	Ser	Asn	Ser	
			200					205					210				
	tca	gga	tct	ggg	gga	ggc	ata	ttt	tct	acc	caa	aca	ctc	acg	atc	tcc	787
	Ser	Gly	Ser	Gly	Gly	Gly	Ile	Phe	Ser	Thr	Gln	Thr	Leu	Thr	Ile	Ser	
		215					220					225					
	tcg	aat	aaa	aaa	ctc	ata	gaa	atc	agt	gaa	aat	tcc	gcg	ttc	gca	aat	835
	Ser	Asn	Lys	Lys	Leu	Ile	Glu	Ile	Ser	Glu	Asn	Ser	Ala	Phe	Ala	Asn	
		230				235					240				245		
50	aac	tat	gga	tcg	aac	ttc	aat	cca	gga	gga	gga	ggg	ctt	act	acc	acc	883
	Asn	Tyr	Gly	Ser	Asn	Phe	Asn	Pro	Gly	Gly	Gly	Gly	Leu	Thr	Thr	Thr	
					250					255					260		
	ttt	tcg	acg	ata	ttg	aac	aac	cga	gaa	ggg	gta	ctc	ttt	aac	aat	aac	931
	Phe	Cys	Thr	Ile	Leu	Asn	Asn	Arg	Glu	Gly	Val	Leu	Phe	Asn	Asn	Asn	
				265				270						275			
60	caa	agc	cag	agc	aac	ggg	gga	gcc	att	cat	gcg	aaa	tct	atc	att	atc	979
	Gln	Ser	Gln	Ser	Asn	Gly	Gly	Ala	Ile	His	Ala	Lys	Ser	Ile	Ile	Ile	
			280					285					290				

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	aaa gaa aat ggt cct gta tac ttt tta aat aac act gca act cgg gga	1027
	Lys Glu Asn Gly Pro Val Tyr Phe Leu Asn Asn Thr Ala Thr Arg Gly	
	295 300 305	
	ggg gct ctc ctc aac tta tca gca ggt tct gga aac gga agc ttc atc	1075
	Gly Ala Leu Leu Asn Leu Ser Ala Gly Ser Gly Asn Gly Ser Phe Ile	
	310 315 320 325	
10	tta tct gca gat aat gga gat att atc ttt aac aat aat acg gcc tcc	1123
	Leu Ser Ala Asp Asn Gly Asp Ile Ile Phe Asn Asn Asn Thr Ala Ser	
	330 335 340	
	aag cat gcc ctc aat cct cca tac aga aac gcc att cac tcg act cct	1171
	Lys His Ala Leu Asn Pro Pro Tyr Arg Asn Ala Ile His Ser Thr Pro	
	345 350 355	
20	aat atg aat ctg caa ata gga gcc cgt ccc ggc tat cga gtg ctg ttc	1219
	Asn Met Asn Asn Leu Gln Ile Gly Ala Arg Pro Gly Tyr Arg Val Leu Phe	
	360 365 370	
	tat gat ccc ata gaa cat gag ctc cct tcc tcc ttc ccc ata ctc ttt	1267
	Tyr Asp Pro Ile Glu His Glu Leu Pro Ser Ser Phe Pro Ile Leu Phe	
	375 380 385	
	aat ttc gaa acc ggt cat aca ggt aca gtt tta ttt tca ggg gaa cat	1315
	Asn Phe Glu Thr Gly His Thr Gly Thr Val Leu Phe Ser Gly Glu His	
	390 395 400 405	
30	gta cac cag aac ttt acc gat gaa atg aat ttc ttt tcc tat tta agg	1363
	Val His Gln Asn Phe Thr Asp Glu Met Asn Phe Phe Ser Tyr Leu Arg	
	410 415 420	
	aac act tcg gaa cta cgt caa gga gtc ctt gct gtt gaa gat ggt gcg	1411
	Asn Thr Ser Glu Leu Arg Gln Gly Val Leu Ala Val Glu Asp Gly Ala	
	425 430 435	
40	ggg ctg gcc tgc tat aag ttc ttc caa cga gga ggc act cta ctt cta	1459
	Gly Leu Ala Cys Tyr Lys Phe Phe Gln Arg Gly Gly Thr Leu Leu Leu	
	440 445 450	
	ggt caa ggt gcg gtg atc acg aca gca gga acg att ccc aca cca tcc	1507
	Gly Gln Gly Ala Val Ile Thr Thr Ala Gly Thr ile Pro Thr Pro Ser	
	455 460 465	
	tca aca cca acg aca gta gga agt act ata act tta aat cac att gcc	1555
	Ser Thr Pro Thr Thr Val Gly Ser Thr Ile Thr Leu Asn His Ile Ala	
	470 475 480 485	
50	att gac ctt cct tct att ctt tct ttt caa gct cag gct cca aaa att	1603
	Ile Asp Leu Pro Ser Ile Leu Ser Phe Gln Ala Gln Ala Pro Lys Ile	
	490 495 500	
	tgg att tac ccc aca aaa aca gga tct acc tat act gaa gat tcc aac	1651
	Trp Ile Tyr Pro Thr Lys Thr Gly Ser Thr Tyr Thr Glu Asp Ser Asn	
	505 510 515	
60	ccg aca atc aca atc tca gga act ctc acc tta cgc aac agc aac aac	1699
	Pro Thr Ile Thr Ile Ser Gly Thr Leu Thr Leu Arg Asn Ser Asn Asn	
	520 525 530	

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		gaa gat ccc tac gat agt ctg gat ctc tcg cac tct ctt gag aaa gtt	1747
		Glu Asp Pro Tyr Asp Ser Leu Asp Leu Ser His Ser Leu Glu Lys Val	
		535 540 545	
10		ccc ctt ctt tat att gtc gat gtc gct gca caa aaa att aac tct tcg	1795
		Pro Leu Leu Tyr Ile Val Asp Val Ala Ala Gln Lys Ile Asn Ser Ser	
		550 555 560 565	
		caa ctg gat cta tcc aca tta aat tct ggc gaa cac tat ggg tat caa	1843
		Gln Leu Asp Leu Ser Thr Leu Asn Ser Gly Glu His Tyr Gly Tyr Gln	
		570 575 580	
		ggc atc tgg tcg acc tat tgg gta gaa act aca aca atc acg aac cct	1891
		Gly Ile Trp Ser Thr Tyr Trp Val Glu Thr Thr Ile Thr Asn Pro	
		585 590 595	
20		aca tct cta cta ggc gcg aat aca aaa cac aag ctg ctc tat gca aac	1939
		Thr Ser Leu Leu Gly Ala Asn Thr Lys His Lys Leu Leu Tyr Ala Asn	
		600 605 610	
		tgg tct cct cta ggc tac cgt cct cat ccc gaa cgt cga gga gaa ttc	1987
		Trp Ser Pro Leu Gly Tyr Arg Pro His Pro Glu Arg Arg Gly Glu Phe	
		615 620 625	
		att acg aat gcc ttg tgg caa tcg gca tat acg gct ctt gca gga ctc	2035
		Ile Thr Asn Ala Leu Trp Gln Ser Ala Tyr Thr Ala Leu Ala Gly Leu	
		630 635 640 645	
30		cac tcc ctc tcc tcc tgg gat gaa gag aag ggt cat gca gct tcc cta	2083
		His Ser Leu Ser Ser Trp Asp Glu Glu Lys Gly His Ala Ala Ser Leu	
		650 655 660	
		caa ggc att ggt ctt ctg gtt cat caa aaa gac aaa aac ggt ttt aag	2131
		Gln Gly Ile Gly Leu Leu Val His Gln Lys Asp Lys Asn Gly Phe Lys	
		665 670 675	
40		gga ttt cgt agt cat atg aca ggt tat agt gct acc acc gaa gca acc	2179
		Gly Phe Arg Ser His Met Thr Gly Tyr Ser Ala Thr Thr Glu Ala Thr	
		680 685 690	
		tct tct caa agt ccg aat ttc tct tta gga ttt gct cag ttc ttc tcc	2227
		Ser Ser Gln Ser Pro Asn Phe Ser Ser Leu Gly Phe Ala Gln Phe Phe Ser	
		695 700 705	
		aaa gct aaa gaa cat gaa tct caa aat agc acg tcc tct cac cac tat	2275
		Lys Ala Lys Glu His Glu Ser Gln Asn Ser Thr Ser Ser His His Tyr	
		710 715 720 725	
50		ttc tct gga atg tgc ata gca aaa tac tct ctt caa aga gtg ata cgt	2323
		Phe Ser Gly Met Cys Ile Ala Lys Tyr Ser Leu Gln Arg Val Ile Arg	
		730 735 740	
		cta tct gtg tct ctt gct tat atg ttt acc tcg gaa cat acc cat aca	2371
		Leu Ser Val Ser Leu Ala Tyr Met Phe Thr Ser Glu His Thr His Thr	
		745 750 755	
60		atg tat cag ggt ctc ctg gaa ggg aac tct cag gga tct ttc cac aac	2419
		Met Tyr Gln Gly Leu Leu Glu Gly Asn Ser Gln Gly Ser Phe His Asn	
		760 765 770	

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cat acc tta gea ggg gct ctc tcc tgt gtt ttc tta cct caa cct cac 2467  
 His Thr Leu Ala Gly Ala Leu Ser Cys Val Phe Leu Pro Gln Pro His  
 775 780 785

ggc gag tcc ctg cag atc tat ccc ttt att act gcc tta gcc atc cga 2515  
 Gly Glu Ser Leu Gln Ile Tyr Pro Phe Ile Thr Ala Leu Ala Ile Arg  
 790 795 800 805

10 gga aat ctt gct gcg ttt caa gaa tct gga gac cat gct cgg gaa ttt 2563  
 Gly Asn Leu Ala Ala Phe Gln Glu Ser Gly Asp His Ala Arg Glu Phe  
 810 815 820

tcc cta cac cgc ccc cta acg gac gtc tcc ctc cct gta gga atc cgc 2611  
 Ser Leu His Arg Pro Leu Thr Asp Val Ser Leu Pro Val Ile Arg  
 825 830 835

20 gct tct tgg aag aac cac cac cga gtt ccc cta gtc tgg ctc aca gaa 2659  
 Ala Ser Trp Lys Asn His His Arg Val Pro Leu Val Trp Leu Thr Glu  
 840 845 850

att tcc tat cgc tct act ctc tat agg caa gat cct gaa ctc cac tcg 2707  
 Ile Ser Tyr Arg Ser Thr Leu Tyr Arg Gln Asp Pro Glu Leu His Ser  
 855 860 865

aaa tta ctg att agc caa ggt acg tgg acg acg cag gcc act cct gtg 2755  
 Lys Leu Leu Ile Ser Gln Gly Thr Trp Thr Thr Gln Ala Thr Pro Val  
 870 875 880 885

30 acc tac aat gct tta ggg atc aaa gtg aaa aat acc atg cag gtg ttt 2803  
 Thr Tyr Asn Ala Leu Gly Ile Lys Val Lys Asn Thr Met Gln Val Phe  
 890 895 900

cct aaa gtc act ctc tcc tta gat tac tct gcg gat att tct tcc tcc 2851  
 Pro Lys Val Thr Leu Ser Leu Asp Tyr Ser Ala Asp Ile Ser Ser Ser  
 905 910 915

40 acg ctg agt cac tac tta aac gtg gcg agt aga atg aga ttt 2893  
 Thr Leu Ser His Tyr Leu Asn Val Ala Ser Arg Met Arg Phe  
 920 925 930

taacaataag tgaccaaacc agaaagatta aggaacctct agtgtcaaag actcctccta 2953  
 agtttttatt ctatctcggg aatttcacag cctgcattgt cgggatg 3000

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 50 <213> Chlamydia pneumoniae

<220>  
 <221> SITE  
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<400> 24  
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 1 5

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<210> 25  
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 <213> Chlamydia pneumoniae

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 <222> (100)..(3033)

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attacgattt taaaccttat ttaacgacag gggtgaggc atg cct ctt tct ttc 114  
 Met Pro Leu Ser Phe 5

aaa tct tca tct ttt tgt cta ctt gcc tgt tta tgt agt gca agt tgc 162  
 Lys Ser Ser Ser Phe Cys Leu Leu Ala Cys Leu Cys Ser Ala Ser Cys 20

gcg ttt gct gag act aga ctc gga ggg aac ttt gtt cct cca att acg 210  
 Ala Phe Ala Glu Thr Arg Leu Gly Gly Asn Phe Val Pro Pro Ile Thr 35

aat cag ggt gaa gag atc tta ctc act tca gat ttt gtt tgt tca aac 258  
 Asn Gln Gly Glu Glu Ile Leu Leu Thr Ser Asp Phe Val Cys Ser Asn 50

ttc ttg ggg gcg agt ttt tca agt tcc ttt atc aat agt tcc agc aat 306  
 Phe Leu Gly Ala Ser Phe Ser Ser Ser Phe Ile Asn Ser Ser Ser Asn 65

ctc tcc tta tta ggg aag ggc ctt tcc tta acg ttt acc tct tgt caa 354  
 Leu Ser Leu Leu Gly Lys Gly Leu Ser Leu Thr Phe Thr Ser Cys Gln 85

gct cct aca aat agt aac tat gcg cta ctt tct gcc gca gag act ctg 402  
 Ala Pro Thr Asn Ser Asn Tyr Ala Leu Leu Ser Ala Ala Glu Thr Leu 100

acc ttc aag aat ttt tct tct ata aac ttt aca ggg aac caa tgc aca 450  
 Thr Phe Lys Asn Phe Ser Ser Ile Asn Phe Thr Gly Asn Gln Ser Thr 115

gga ctt ggc ggc ctc atc tac gga aaa gat att gtt ttc caa tct atc 498  
 Gly Leu Gly Gly Leu Ile Tyr Gly Lys Asp Ile Val Phe Gln Ser Ile 130

aaa gat ttg atc ttc act acg aac cgt gtt gcc tat tct cca gca tct 546  
 Lys Asp Leu Ile Phe Thr Thr Asn Arg Val Ala Tyr Ser Pro Ala Ser 145

gta act acg tgc gca act ccc gca atc act aca gta act aca gga gcc 594  
 Val Thr Thr Ser Ala Thr Pro Ala Ile Thr Thr Val Thr Thr Gly Ala 165

tct gct ctc caa cct aca gac tca ctc act gtc gaa aac ata tcc caa 642  
 Ser Ala Leu Gln Pro Thr Asp Ser Leu Thr Val Glu Asn Ile Ser Gln 180

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	tcg atc aag ttt ttt ggg aac ctt gcc aac ttc ggc tct gca att agc	690
	Ser Ile Lys Phe Phe Gly Asn Leu Ala Asn Phe Gly Ser Ala Ile Ser	
	185 190 195	
	agt tct ccc acg gca gtc gtt aaa ttc atc aat aac acc gct acc atg	738
	Ser Ser Pro Thr Ala Val Val Lys Phe Ile Asn Asn Thr Ala Thr Met	
	200 205 210	
10	agc ttc tcc cat aac ttt act tcg tca gga ggc ggc gtg att tat gga	786
	Ser Phe Ser His Asn Phe Thr Ser Ser Gly Gly Val Ile Tyr Gly	
	215 220 225	
	gga agc tct ctc ctt ttt gaa aac aat tct gga tgc atc atc ttc acc	834
	Gly Ser Ser Leu Leu Phe Glu Asn Asn Ser Gly Cys Ile Ile Phe Thr	
	230 235 240 245	
20	gcc aac tcc tgt gtg aac agc tta aaa ggc gtc acc cct tca tca gga	882
	Ala Asn Ser Cys Val Asn Ser Leu Lys Gly Val Thr Pro Ser Ser Gly	
	250 255 260	
	acc tat gct tta gga agt ggc gga gcc atc tgc atc cct acg gga act	930
	Thr Tyr Ala Leu Gly Ser Gly Gly Ala Ile Cys Ile Pro Thr Gly Thr	
	265 270 275	
	ttc gaa tta aaa aac aat cag ggg aag tgc acc ttc tct tat aat ggt	978
	Phe Glu Leu Lys Asn Asn Gln Gly Lys Cys Thr Phe Ser Tyr Asn Gly	
	280 285 290	
30	aca cca aat gat gcg ggt gcg atc tac gcc gaa acc tgc aac atc gta	1026
	Thr Pro Asn Asp Ala Gly Ala Ile Tyr Ala Glu Thr Cys Asn Ile Val	
	295 300 305	
	ggg aac cag ggt gcc ttg ctc cta gat agc aac act gca gcg aga aat	1074
	Gly Asn Gln Gly Ala Leu Leu Leu Asp Ser Asn Thr Ala Ala Arg Asn	
	310 315 320 325	
40	ggc gga gcc atc tgt gct aaa gtg ctc aat att caa gga cgc ggt cct	1122
	Gly Gly Ala Ile Cys Ala Lys Val Leu Asn Ile Gln Gly Arg Gly Pro	
	330 335 340	
	att gaa ttc tct aga aac cgc gcg gag aag ggt gga gct att ttc ata	1170
	Ile Glu Phe Ser Arg Asn Arg Ala Glu Lys Gly Gly Ala Ile Phe Ile	
	345 350 355	
	ggc ccc tct gtt gga gac cct gcg aag caa aca tcg aca ctt acg att	1218
	Gly Pro Ser Val Gly Asp Pro Ala Lys Gln Thr Ser Thr Leu Thr Ile	
	360 365 370	
50	ttg gct tcc gaa ggt gat att gcg ttc caa gga aac atg ctc aat aca	1266
	Leu Ala Ser Glu Gly Asp Ile Ala Phe Gln Gly Asn Met Leu Asn Thr	
	375 380 385	
	aaa cct gga atc cgc aat gcc atc act gta gaa gca ggg gga gag att	1314
	Lys Pro Gly Ile Arg Asn Ala Ile Thr Val Glu Ala Gly Gly Glu Ile	
	390 395 400 405	
60	gtg tct cta tct gca caa gga ggc tca cgt ett gta ttt tat gat ccc	1362
	Val Ser Leu Ser Ala Gln Gly Gly Ser Arg Leu Val Phe Tyr Asp Pro	
	410 415 420	



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	att aca cat agc ctc cca acc aca agt ccg tct aat aaa gac att aca	1410
	Ile Thr His Ser Leu Pro Thr Thr Ser Pro Ser Asn Lys Asp Ile Thr	
	425 430 435	
	atc aac gct aat ggc gct tca gga tct gta gtc ttt aca agt aag gga	1458
	Ile Asn Ala Asn Gly Ala Ser Gly Ser Val Val Phe Thr Ser Lys Gly	
	440 445 450	
10	ctc tcc tct aca gaa ctc ctg ttg cct gcc aac acg aca act ata ctt	1506
	Leu Ser Ser Thr Glu Leu Leu Pro Ala Asn Thr Thr Thr Ile Leu	
	455 460 465	
	cta gga aca gtc aag atc gct agt gga gaa ctg aag att act gac aat	1554
	Leu Gly Thr Val Lys Ile Ala Ser Gly Glu Leu Lys Ile Thr Asp Asn	
	470 475 480 485	
20	gcg gtt gtc aat gtt gct ggc ttc gct act cag ggc tca ggt cag ctt	1602
	Ala Val Val Asn Val Ala Gly Phe Ala Thr Gln Gly Ser Gly Gln Leu	
	490 495 500	
	acc ctg ggc tct gga gga acc tta ggg ctg gca aca ccc acg gga gca	1650
	Thr Leu Gly Ser Gly Gly Thr Leu Gly Leu Ala Thr Pro Thr Gly Ala	
	505 510 515	
	cct gcc gct gta gac ttt acg att gga aag tta gca ttc gat cct ttt	1698
	Pro Ala Ala Val Asp Phe Thr Ile Gly Lys Leu Ala Phe Asp Pro Phe	
	520 525 530	
30	tcc ttc cta aaa aga gat ttt gtt tca gca tca gta aat gca ggc aca	1746
	Ser Phe Leu Lys Arg Asp Phe Val Ser Ala Ser Val Asn Ala Gly Thr	
	535 540 545	
	aaa aac gtc act tta aca gga gct ctg gtt ctt gat gaa cat gac gtt	1794
	Lys Asn Val Thr Leu Thr Gly Ala Leu Val Leu Asp Glu His Asp Val	
	550 555 560 565	
40	aca gat ctt tat gat atg gtg tca tta caa tct cca gta gca att cct	1842
	Thr Asp Leu Tyr Asp Met Val Ser Leu Gln Ser Pro Val Ala Ile Pro	
	570 575 580	
	atc gct gtt ttc aaa gga gca acc gtt act aag aca gga ttt cct gat	1890
	Ile Ala Val Phe Lys Gly Ala Thr Val Thr Lys Thr Gly Phe Pro Asp	
	585 590 595	
	ggg gag att gcg act cca agc cac tac ggc tac caa gga aag tgg tcc	1938
	Gly Glu Ile Ala Thr Pro Ser His Tyr Gly Tyr Gln Gly Lys Trp Ser	
	600 605 610	
50	tac aca tgg tcc cgt ccc ctg tta att cca gct cct gat gga gga ttt	1986
	Tyr Thr Trp Ser Arg Pro Leu Leu Ile Pro Ala Pro Asp Gly Gly Phe	
	615 620 625	
	cct gga ggt ccc tct cct agc gca aat act ctc tat gct gta tgg aat	2034
	Pro Gly Gly Pro Ser Pro Ser Ala Asn Thr Leu Tyr Ala Val Trp Asn	
	630 635 640 645	
60	tca gac act ctc gtg cgt tct acc tat atc tta gat ccc gag cgt tac	2082
	Ser Asp Thr Leu Val Arg Ser Thr Tyr Ile Leu Asp Pro Glu Arg Tyr	
	650 655 660	

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	gga gaa att gtc agc aac agc tta tgg att tcc ttc tta gga aat cag	2130
	Gly Glu Ile Val Ser Asn Ser Leu Trp Ile Ser Phe Leu Gly Asn Gln	
	665 670 675	
	gca ttc tct gat att ctc caa gat gtt ctt ttg ata gat cat ccc ggg	2178
	Ala Phe Ser Asp Ile Leu Gln Asp Val Leu Leu Ile Asp His Pro Gly	
	680 685 690	
10	ttg tcc ata acc gcg aaa gct tta gga gcc tat gtc gaa cac aca cca	2226
	Leu Ser Ile Thr Ala Lys Ala Leu Gly Ala Tyr Val Glu His Thr Pro	
	695 700 705	
	aga caa gga cat gag ggc ttt tca ggt cgc tat gga ggc tac caa gct	2274
	Arg Gln Gly His Glu Gly Phe Ser Gly Arg Tyr Gly Gly Tyr Gln Ala	
	710 715 720 725	
20	gcg cta tct atg aac tac acg gac cac act acg tta gga ctt tct ttc	2322
	Ala Leu Ser Met Asn Tyr Thr Asp His Thr Thr Leu Gly Leu Ser Phe	
	730 735 740	
	ggg cag ctt tat gga aaa act aac gcc aac ccc tac gat tca cgt tgc	2370
	Gly Gln Leu Tyr Gly Lys Thr Asn Ala Asn Pro Tyr Asp Ser Arg Cys	
	745 750 755	
	tca gaa caa atg tat tta ctc tcg ttc ttt ggt caa ttc cct atc gtg	2418
	Ser Glu Gln Met Tyr Leu Leu Ser Phe Phe Gly Gln Phe Pro Ile Val	
	760 765 770	
30	act caa aag agc gag gcc tta att tcc tgg aaa gca gct tat ggt tat	2466
	Thr Gln Lys Ser Glu Ala Leu Ile Ser Trp Lys Ala Ala Tyr Gly Tyr	
	775 780 785	
	tcc aaa aat cac cta aat acc acc tac ctc aga cct gac aaa gct cca	2514
	Ser Lys Asn His Leu Asn Thr Thr Tyr Leu Arg Pro Asp Lys Ala Pro	
	790 795 800 805	
40	aaa tct caa ggg caa tgg cat aac aat agt tac tat gtt ctt att tct	2562
	Lys Ser Gln Gly Gln Trp His Asn Asn Ser Tyr Tyr Val Leu Ile Ser	
	810 815 820	
	gca gaa cat cct ttc cta aac tgg tgt ctt ctt aca aga cct ctg gct	2610
	Ala Glu His Pro Phe Leu Asn Trp Cys Leu Leu Thr Arg Pro Leu Ala	
	825 830 835	
	caa gct tgg gat ctt tca ggt ttt att tcc gca gaa ttc cta ggt ggt	2658
	Gln Ala Trp Asp Leu Ser Gly Phe Ile Ser Ala Glu Phe Leu Gly Gly	
	840 845 850	
50	tgg caa agt aag ttc aca gaa act gga gat ctg caa cgt agc ttt agt	2706
	Trp Gln Ser Lys Phe Thr Glu Thr Gly Asp Leu Gln Arg Ser Phe Ser	
	855 860 865	
	aga ggt aaa ggg tac aat gtt tcc cta ccg ata gga tgt tct tct caa	2754
	Arg Gly Lys Gly Tyr Asn Val Ser Leu Pro Ile Gly Cys Ser Ser Gln	
	870 875 880 885	
60	tgg ttc aca cca ttt aag aag gct cct tct aca ctg acc atc aaa ctt	2802
	Trp Phe Thr Pro Phe Lys Lys Ala Pro Ser Thr Leu Thr Ile Lys Leu	
	890 895 900	

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gcc tac aag cct gat atc tat cgt gtc aac cct cac aat att gtg act 2850
Ala Tyr Lys Pro Asp Ile Tyr Arg Val Asn Pro His Asn Ile Val Thr
          905                      910                      915

gtc gtc tca aac caa gag agc act tcg atc tca gga gca aat cta cgc 2898
Val Val Ser Asn Gln Glu Ser Thr Ser Ile Ser Gly Ala Asn Leu Arg
          920                      925                      930

10  cgc cac ggt ttg ttt gta caa atc cat gat gta gta gat ctc acc gag 2946
Arg His Gly Leu Phe Val Gln Ile His Asp Val Val Asp Leu Thr Glu
          935                      940                      945

gac act cag gcc ttt cta aac tat acc ttt gac ggg aaa aat gga ttt 2994
Asp Thr Gln Ala Phe Leu Asn Tyr Thr Phe Asp Gly Lys Asn Gly Phe
          950                      955                      960

20  aca aac cac cga gtg tct aca gga cta aaa tcc aca ttt taaaactcta 3043
Thr Asn His Arg Val Ser Thr Gly Leu Lys Ser Thr Phe
          970                      975

agctctgctt agagttttct gtagcccccgg tcgtcttaga atcctctatc catcatcgaa 3103
gaacttagca atgaaggcca agattctcac tctatgagaa cccccccc 3150

<210> 26
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30  <213> Chlamydia pneumoniae

<220>
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<222> (936)..(944)

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Gly Leu Phe Val Gln Ile His Asp Val
1          5

40  <210> 27
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<212> PRT
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Met Lys Ile Pro Leu Arg Phe Leu Leu Ile Ser Leu Val Pro Thr Leu
1          5          10          15

50  Ser Met Ser Asn Leu Leu Gly Ala Ala Thr Thr Glu Glu Leu Ser Ala
          20          25          30

Ser Asn Ser Phe Asp Gly Thr Thr Ser Thr Thr Ser Phe Ser Ser Lys
          35          40          45

Thr Ser Ser Ala Thr Asp Gly Thr Asn Tyr Val Phe Lys Asp Ser Val
          50          55          60

60  Val Ile Glu Asn Val Pro Lys Thr Gly Glu Thr Gln Ser Thr Ser Cys
          65          70          75          80

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Phe Lys Asn Asp Ala Ala Ala Gly Asp Leu Asn Phe Leu Gly Gly Gly  
                     85                    90                    95  
 Phe Ser Phe Thr Phe Ser Asn Ile Asp Ala Thr Thr Ala Ser Gly Ala  
                     100                    105                    110  
 Ala Ile Gly Ser Glu Ala Ala Asn Lys Thr Val Thr Leu Ser Gly Phe  
                     115                    120                    125  
 10 Ser Ala Leu Ser Phe Leu Lys Ser Pro Ala Ser Thr Val Thr Asn Gly  
                     130                    135                    140  
 Leu Gly Ala Ile Asn Val Lys Gly Asn Leu Ser Leu Leu Asp Asn Asp  
                     145                    150                    155                    160  
 Lys Val Leu Ile Gln Asp Asn Phe Ser Thr Gly Asp Gly Gly Ala Ile  
                     165                    170                    175  
 20 Asn Cys Ala Gly Ser Leu Lys Ile Ala Asn Asn Lys Ser Leu Ser Phe  
                     180                    185                    190  
 Ile Gly Asn Ser Ser Ser Thr Arg Gly Gly Ala Ile His Thr Lys Asn  
                     195                    200                    205  
 Leu Thr Leu Ser Ser Gly Gly Glu Thr Leu Phe Gln Gly Asn Thr Ala  
                     210                    215                    220  
 30 Pro Thr Ala Ala Gly Lys Gly Gly Ala Ile Ala Ile Ala Asp Ser Gly  
                     225                    230                    235                    240  
 Thr Leu Ser Ile Ser Gly Asp Ser Gly Asp Ile Ile Phe Glu Gly Asn  
                     245                    250                    255  
 Thr Ile Gly Ala Thr Gly Thr Val Ser His Ser Ala Ile Asp Leu Gly  
                     260                    265                    270  
 Thr Ser Ala Lys Ile Thr Ala Leu Arg Ala Ala Gln Gly His Thr Ile  
                     275                    280                    285  
 40 Tyr Phe Tyr Asp Pro Ile Thr Val Thr Gly Ser Thr Ser Val Ala Asp  
                     290                    295                    300  
 Ala Leu Asn Ile Asn Ser Pro Asp Thr Gly Asp Asn Lys Glu Tyr Thr  
                     305                    310                    315                    320  
 Gly Thr Ile Val Phe Ser Gly Glu Lys Leu Thr Glu Ala Glu Ala Lys  
                     325                    330                    335  
 50 Asp Glu Lys Asn Arg Thr Ser Lys Leu Leu Gln Asn Val Ala Phe Lys  
                     340                    345                    350  
 Asn Gly Thr Val Val Leu Lys Gly Asp Val Val Leu Ser Ala Asn Gly  
                     355                    360                    365  
 Phe Ser Gln Asp Ala Asn Ser Lys Leu Ile Met Asp Leu Gly Thr Ser  
                     370                    375                    380  
 60 Leu Val Ala Asn Thr Glu Ser Ile Glu Leu Thr Asn Leu Glu Ile Asn  
                     385                    390                    395                    400

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Ile Asp Ser Leu Arg Asn Gly Lys Lys Ile Lys Leu Ser Ala Ala Thr  
 405 410 415  
 Ala Gln Lys Asp Ile Arg Ile Asp Arg Pro Val Val Leu Ala Ile Ser  
 420 425 430  
 10 Asp Glu Ser Phe Tyr Gln Asn Gly Phe Leu Asn Glu Asp His Ser Tyr  
 435 440 445  
 Asp Gly Ile Leu Glu Leu Asp Ala Gly Lys Asp Ile Val Ile Ser Ala  
 450 455 460  
 Asp Ser Arg Ser Ile Asp Ala Val Gln Ser Pro Tyr Gly Tyr Gln Gly  
 465 470 475 480  
 Lys Trp Thr Ile Asn Trp Ser Thr Asp Asp Lys Lys Ala Thr Val Ser  
 485 490 495  
 20 Trp Ala Lys Gln Ser Phe Asn Pro Thr Ala Glu Gln Glu Ala Pro Leu  
 500 505 510  
 Val Pro Asn Leu Leu Trp Gly Ser Phe Ile Asp Val Arg Ser Phe Gln  
 515 520 525  
 Asn Phe Ile Glu Leu Gly Thr Glu Gly Ala Pro Tyr Glu Lys Arg Phe  
 530 535 540  
 30 Trp Val Ala Gly Ile Ser Asn Val Leu His Arg Ser Gly Arg Glu Asn  
 545 550 555 560  
 Gln Arg Lys Phe Arg His Val Ser Gly Gly Ala Val Val Gly Ala Ser  
 565 570 575  
 Thr Arg Met Pro Gly Gly Asp Thr Leu Ser Leu Gly Phe Ala Gln Leu  
 580 585 590  
 40 Phe Ala Arg Asp Lys Asp Tyr Phe Met Asn Thr Asn Phe Ala Lys Thr  
 595 600 605  
 Tyr Ala Gly Ser Leu Arg Leu Gln His Asp Ala Ser Leu Tyr Ser Val  
 610 615 620  
 Val Ser Ile Leu Leu Gly Glu Gly Gly Leu Arg Glu Ile Leu Leu Pro  
 625 630 635 640  
 Tyr Val Ser Lys Thr Leu Pro Cys Ser Phe Tyr Gly Gln Leu Ser Tyr  
 645 650 655  
 50 Gly His Thr Asp His Arg Met Lys Thr Glu Ser Leu Pro Pro Pro Pro  
 660 665 670  
 Pro Thr Leu Ser Thr Asp His Thr Ser Trp Gly Gly Tyr Val Trp Ala  
 675 680 685  
 Gly Glu Leu Gly Thr Arg Val Ala Val Glu Asn Thr Ser Gly Arg Gly  
 690 695 700  
 60 Phe Phe Gln Glu Tyr Thr Pro Phe Val Lys Val Gln Ala Val Tyr Ala  
 705 710 715 720

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Arg Gln Asp Ser Phe Val Glu Leu Gly Ala Ile Ser Arg Asp Phe Ser  
                             725                            730                            735  
 Asp Ser His Leu Tyr Asn Leu Ala Ile Pro Leu Gly Ile Lys Leu Glu  
                             740                            745                            750  
 10 Lys Arg Phe Ala Glu Gln Tyr Tyr His Val Val Ala Met Tyr Ser Pro  
                             755                            760                            765  
 Asp Val Cys Arg Ser Asn Pro Lys Cys Thr Thr Thr Leu Leu Ser Asn  
                             770                            775                            780  
 Gln Gly Ser Trp Lys Thr Lys Gly Ser Asn Leu Ala Arg Gln Ala Gly  
                             785                            790                            795                            800  
 20 Ile Val Gln Ala Ser Gly Phe Arg Ser Leu Gly Ala Ala Ala Glu Leu  
                             805                            810                            815  
 Phe Gly Asn Phe Gly Phe Glu Trp Arg Gly Ser Ser Arg Ser Tyr Asn  
                             820                            825                            830  
 Val Asp Ala Gly Ser Lys Ile Lys Phe  
                             835                            840  
 30 <210> 28  
       <211> 841  
       <212> PRT  
       <213> Chlamydia pneumoniae  
       <400> 28  
       Met Lys Ile Pro Leu Arg Phe Leu Leu Ile Ser Leu Val Pro Thr Leu  
           1                            5                            10                            15  
       Ser Met Ser Asn Leu Leu Gly Ala Ala Thr Thr Glu Glu Leu Ser Ala  
                             20                            25                            30  
 40 Ser Asn Ser Phe Asp Gly Thr Thr Ser Thr Thr Ser Phe Ser Ser Lys  
                             35                            40                            45  
       Thr Ser Ser Ala Thr Asp Gly Thr Asn Tyr Val Phe Lys Asp Ser Val  
           50                            55                            60  
       Val Ile Glu Asn Val Pro Lys Thr Gly Glu Thr Gln Ser Thr Ser Cys  
           65                            70                            75                            80  
 50 Phe Lys Asn Asp Ala Ala Ala Gly Asp Leu Asn Phe Leu Gly Gly Gly  
                             85                            90                            95  
       Phe Ser Phe Thr Phe Ser Asn Ile Asp Ala Thr Thr Ala Ser Gly Ala  
           100                            105                            110  
       Ala Ile Gly Ser Glu Ala Ala Asn Lys Thr Val Thr Leu Ser Gly Phe  
           115                            120                            125  
       Ser Ala Leu Ser Phe Leu Lys Ser Pro Ala Ser Thr Val Thr Asn Gly  
           130                            135                            140  
 60

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Leu Gly Ala Ile Asn Val Lys Gly Asn Leu Ser Leu Leu Asp Asn Asp  
 145 150 155 160  
 Lys Val Leu Ile Gln Asp Asn Phe Ser Thr Gly Asp Gly Gly Ala Ile  
 165 170 175  
 10 Asn Cys Ala Gly Ser Leu Lys Ile Ala Asn Asn Lys Ser Leu Ser Phe  
 180 185 190  
 Ile Gly Asn Ser Ser Ser Thr Arg Gly Gly Ala Ile His Thr Lys Asn  
 195 200 205  
 Leu Thr Leu Ser Ser Gly Gly Glu Thr Leu Phe Gln Gly Asn Thr Ala  
 210 215 220  
 20 Pro Thr Ala Ala Gly Lys Gly Gly Ala Ile Ala Ile Ala Asp Ser Gly  
 225 230 235 240  
 Thr Leu Ser Ile Ser Gly Asp Ser Gly Asp Ile Ile Phe Glu Gly Asn  
 245 250 255  
 Thr Ile Gly Ala Thr Gly Thr Val Ser His Ser Ala Ile Asp Leu Gly  
 260 265 270  
 Thr Ser Ala Lys Ile Thr Ala Leu Arg Ala Ala Gln Gly His Thr Ile  
 275 280 285  
 30 Tyr Phe Tyr Asp Pro Ile Thr Val Thr Gly Ser Thr Ser Val Ala Asp  
 290 295 300  
 Ala Leu Asn Ile Asn Ser Pro Asp Thr Gly Asp Asn Lys Glu Tyr Thr  
 305 310 315 320  
 Gly Thr Ile Val Phe Ser Gly Glu Lys Leu Thr Glu Ala Glu Ala Lys  
 325 330 335  
 40 Asp Glu Lys Asn Arg Thr Ser Lys Leu Leu Gln Asn Val Ala Phe Lys  
 340 345 350  
 Asn Gly Thr Val Val Leu Lys Gly Asp Val Val Leu Ser Ala Asn Gly  
 355 360 365  
 Phe Ser Gln Asp Ala Asn Ser Lys Leu Ile Met Asp Leu Gly Thr Ser  
 370 375 380  
 Leu Val Ala Asn Thr Glu Ser Ile Glu Leu Thr Asn Leu Glu Ile Asn  
 385 390 395 400  
 50 Ile Asp Ser Leu Arg Asn Gly Lys Lys Ile Lys Leu Ser Ala Ala Thr  
 405 410 415  
 Ala Gln Lys Asp Ile Arg Ile Asp Arg Pro Val Val Leu Ala Ile Ser  
 420 425 430  
 Asp Glu Ser Phe Tyr Gln Asn Gly Phe Leu Asn Glu Asp His Ser Tyr  
 435 440 445  
 60 Asp Gly Ile Leu Glu Leu Asp Ala Gly Lys Asp Ile Val Ile Ser Ala  
 450 455 460

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	Asp Ser Arg Ser Ile	Asp Ala Val Gln Ser	Pro Tyr Gly Tyr Gln Gly
	465	470	475 480
	Lys Trp Thr Ile Asn Trp Ser Thr	Asp Asp Lys Lys Ala Thr Val Ser	
		485 490 495	
10	Trp Ala Lys Gln Ser Phe Asn Pro Thr	Ala Glu Gln Glu Ala Pro Leu	
		500 505 510	
	Val Pro Asn Leu Leu Trp Gly Ser Phe Ile Asp Val Arg Ser Phe Gln		
		515 520 525	
	Asn Phe Ile Glu Leu Gly Thr Glu Gly Ala Pro Tyr Glu Lys Arg Phe		
		530 535 540	
20	Trp Val Ala Gly Ile Ser Asn Val Leu His Arg Ser Gly Arg Glu Asn		
		545 550 555 560	
	Gln Arg Lys Phe Arg His Val Ser Gly Gly Ala Val Val Gly Ala Ser		
		565 570 575	
	Thr Arg Met Pro Gly Gly Asp Thr Leu Ser Leu Gly Phe Ala Gln Leu		
		580 585 590	
	Phe Ala Arg Asp Lys Asp Tyr Phe Met Asn Thr Asn Phe Ala Lys Thr		
		595 600 605	
30	Tyr Ala Gly Ser Leu Arg Leu Gln His Asp Ala Ser Leu Tyr Ser Val		
		610 615 620	
	Val Ser Ile Leu Leu Gly Glu Gly Leu Arg Glu Ile Leu Leu Pro		
		625 630 635 640	
	Tyr Val Ser Lys Thr Leu Pro Cys Ser Phe Tyr Gly Gln Leu Ser Tyr		
		645 650 655	
40	Gly His Thr Asp His Arg Met Lys Thr Glu Ser Leu Pro Pro Pro Pro		
		660 665 670	
	Pro Thr Leu Ser Thr Asp His Thr Ser Trp Gly Gly Tyr Val Trp Ala		
		675 680 685	
	Gly Glu Leu Gly Thr Arg Val Ala Val Glu Asn Thr Ser Gly Arg Gly		
		690 695 700	
50	Phe Phe Gln Glu Tyr Thr Pro Phe Val Lys Val Gln Ala Val Tyr Ala		
		705 710 715 720	
	Arg Gln Asp Ser Phe Val Glu Leu Gly Ala Ile Ser Arg Asp Phe Ser		
		725 730 735	
	Asp Ser His Leu Tyr Asn Leu Ala Ile Pro Leu Gly Ile Lys Leu Glu		
		740 745 750	
	Lys Arg Phe Ala Glu Gln Tyr Tyr His Val Val Ala Met Tyr Ser Pro		
		755 760 765	
60	Asp Val Cys Arg Ser Asn Pro Lys Cys Thr Thr Thr Leu Leu Ser Asn		
		770 775 780	





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Gln Met Met Met Leu Ser Pro Leu Ser Ile Ser Leu Pro Leu Lys Leu  
 210 215 220  
 Leu Leu Ile Val Met Val Asp Gly Trp Thr Leu Leu Leu Gln Gly Leu  
 225 230 235 240  
 Met Ile Ser Phe Lys  
 245  
 <210> 30  
 <211> 233  
 <212> PRT  
 <213> Chlamydia pneumoniae  
 <400> 30  
 Met Lys Phe Phe Ser Leu Ile Phe Lys Asp Asp Asp Val Ser Pro Asn  
 1 5 10 15  
 Lys Lys Val Leu Ser Pro Glu Ala Phe Ser Ala Phe Leu Asp Ala Lys  
 20 25 30  
 Glu Leu Leu Glu Lys Thr Lys Ala Asp Ser Glu Ala Tyr Val Ala Glu  
 35 40 45  
 Thr Glu Gln Lys Cys Ala Gln Ile Arg Gln Glu Ala Lys Asp Gln Gly  
 50 55 60  
 Phe Lys Glu Gly Ser Glu Ser Trp Ser Lys Gln Ile Ala Phe Leu Glu  
 65 70 75 80  
 Glu Glu Thr Lys Asn Leu Arg Ile Arg Val Arg Glu Ala Leu Val Pro  
 85 90 95  
 Leu Ala Ile Ala Ser Val Arg Lys Ile Ile Gly Lys Glu Leu Glu Leu  
 100 105 110  
 His Pro Glu Thr Ile Val Ser Ile Ile Ser Gln Ala Leu Lys Glu Leu  
 115 120 125  
 Thr Gln Asn Lys His Ile Ile Ile Ser Val Asn Pro Lys Asp Leu Pro  
 130 135 140  
 Leu Val Glu Lys Ser Arg Pro Glu Leu Lys Asn Ile Val Glu Tyr Ala  
 145 150 155 160  
 Asp Ser Leu Ile Leu Thr Ala Lys Pro Asp Val Thr Pro Gly Gly Cys  
 165 170 175  
 Ile Ile Glu Thr Glu Ala Gly Ile Ile Asn Ala Gln Leu Asp Val Gln  
 180 185 190  
 Leu Asp Ala Leu Glu Lys Ala Phe Ser Thr Ile Leu Lys Ala Lys Asn  
 195 200 205  
 Pro Val Asp Glu Pro Ser Glu Thr Ser Ser Ser Thr Asp Ser Ser Ser  
 210 215 220

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Leu Ser Asn Asp Gln Asp Lys Lys Glu  
 225 230

<210> 31

<211> 322

<212> PRT

10 <213> Chlamydia pneumoniae

<400> 31

Met Thr Leu Leu Cys Cys Thr Ser Cys Asn Ser Arg Ser Leu Ile Val  
 1 5 10 15

His Gly Leu Pro Gly Arg Glu Ala Asn Glu Ile Val Val Leu Leu Val  
 20 25 30

20 Ser Lys Gly Val Ala Ala Gln Lys Leu Pro Gln Ala Ala Ala Thr  
 35 40 45

Ala Gly Ala Ala Thr Glu Gln Met Trp Asp Ile Ala Val Pro Ser Ala  
 50 55 60

Gln Ile Thr Glu Ala Leu Ala Ile Leu Asn Gln Ala Gly Leu Pro Arg  
 65 70 75 80

Met Lys Gly Thr Ser Leu Leu Asp Leu Phe Ala Lys Gln Gly Leu Val  
 85 90 95

30 Pro Ser Glu Leu Gln Glu Lys Ile Arg Tyr Gln Glu Gly Leu Ser Glu  
 100 105 110

Gln Met Ala Ser Thr Ile Arg Lys Met Asp Gly Val Val Asp Ala Ser  
 115 120 125

Val Gln Ile Ser Phe Thr Thr Glu Asn Glu Asp Asn Leu Pro Leu Thr  
 130 135 140

40 Ala Ser Val Tyr Ile Lys His Arg Gly Val Leu Asp Asn Pro Asn Ser  
 145 150 155 160

Ile Met Val Ser Lys Ile Lys Arg Leu Ile Ala Ser Ala Val Pro Gly  
 165 170 175

Leu Val Pro Glu Asn Val Ser Val Val Ser Asp Arg Ala Ala Tyr Ser  
 180 185 190

50 Asp Ile Thr Ile Asn Gly Pro Trp Gly Leu Thr Glu Glu Ile Asp Tyr  
 195 200 205

Val Ser Val Trp Gly Ile Ile Leu Ala Lys Ser Ser Leu Thr Lys Phe  
 210 215 220

Arg Leu Ile Phe Tyr Val Leu Ile Leu Ile Leu Phe Val Ile Ser Cys  
 225 230 235 240

Gly Leu Leu Trp Val Ile Trp Lys Thr His Thr Leu Ile Met Thr Met  
 245 250 255

60

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Gly Gly Thr Lys Gly Phe Phe Asn Pro Thr Pro Tyr Thr Lys Asn Ala  
 260 265 270  
 Leu Glu Ala Lys Lys Ala Glu Gly Ala Ala Ala Asp Lys Glu Lys Lys  
 275 280 285  
 10 Gly Asp Ala Asp Ser Gln Gly Glu Ser Lys Asn Ala Glu Thr Ser Asp  
 290 295 300  
 Lys Asp Ser Ser Asp Lys Asp Ala Pro Glu Gly Ser Asn Glu Ile Glu  
 305 310 315 320  
 Gly Ala  
 <210> 32  
 <211> 226  
 20 <212> PRT  
 <213> Chlamydia pneumoniae  
 <400> 32  
 Met Thr Ile Arg Val Arg Asn Leu Ala Tyr Ser Val Asn Lys Lys Lys  
 1 5 10 15  
 Ile Leu Asp Gly Val Thr Phe Ser Leu Glu Arg Gly His Ile Thr Leu  
 20 25 30  
 30 Phe Val Gly Lys Ser Gly Ser Gly Lys Thr Met Ile Leu Arg Ala Leu  
 35 40 45  
 Ala Gly Leu Val Gln Pro Thr Gln Gly Asp Ile Trp Ile Glu Gly Glu  
 50 55 60  
 Ala Pro Ala Leu Val Phe Gln Gln Pro Glu Leu Phe Ser His Met Thr  
 65 70 75 80  
 40 Val Leu Gly Asn Cys Thr His Pro Gln Ile His Ile Lys Gly Arg Ser  
 85 90 95  
 Thr Glu Glu Ala Arg Glu Lys Ala Phe Glu Leu Leu His Leu Leu Asp  
 100 105 110  
 Ile Glu Glu Val Ala Lys Asn Tyr Pro Asp Gln Leu Ser Gly Gly Gln  
 115 120 125  
 Lys Gln Arg Val Ala Ile Val Arg Ser Leu Cys Met Asp Lys His Thr  
 130 135 140  
 50 Leu Leu Phe Asp Glu Pro Thr Ser Ala Leu Asp Pro Phe Ala Thr Ala  
 145 150 155 160  
 Ser Phe Arg His Leu Leu Glu Thr Leu Arg Asp Gln Glu Leu Thr Val  
 165 170 175  
 Gly Leu Thr Thr His Asp Met Gln Phe Val His Ser Cys Leu Asp Arg  
 180 185 190  
 60 Ile Tyr Leu Ile Asp Gln Gly Thr Val Ala Gly Val Tyr Asp Lys Arg  
 195 200 205

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Asp Gly Glu Leu Asp Ser Gly His Pro Leu Ser Lys Tyr Ile His Ser  
 210 215 220

Ala Gln  
 225

10 <210> 33  
 <211> 436  
 <212> PRT  
 <213> Chlamydia pneumoniae  
 <400> 33  
 Met Lys Arg Pro Phe Phe Thr Tyr Leu Cys Ile Ile Phe Tyr Gly Ser  
 1 5 10 15  
 20 Cys Ala Ser Leu Ser Leu His Ala Gly Leu Ser Phe Pro Glu Val Arg  
 20 25 30  
 Gly Ala Thr Ala Ala Val Val His Ala Asp Ser Gly Lys Val Phe Tyr  
 35 40 45  
 Asp Lys Asp Ile Asp Ala Val Ile Tyr Pro Ala Ser Met Thr Lys Ile  
 50 55 60  
 Ala Thr Ala Leu Phe Ile Leu Lys His Tyr Pro Thr Val Leu Asp Thr  
 65 70 75 80  
 30 Leu Ile Lys Val Lys Gln Asp Ala Ile Ala Ser Ile Thr Pro Gln Ala  
 85 90 95  
 Lys Lys Gln Ser Gly Tyr Arg Ser Pro Pro His Trp Leu Glu Thr Asp  
 100 105 110  
 Gly Ser Thr Ile Gln Leu His Leu Arg Glu Glu Leu Leu Gly Trp Asp  
 115 120 125  
 40 Leu Phe His Ala Leu Leu Val Cys Ser Ala Asn Asp Ala Ala Asn Val  
 130 135 140  
 Leu Ala Met Ala Cys Cys Gly Ser Val Glu Lys Phe Met Asp Lys Leu  
 145 150 155 160  
 Asn Phe Phe Leu Lys Glu Glu Ile Gly Cys Thr His Thr His Phe Asn  
 165 170 175  
 50 Asn Pro His Gly Leu His His Pro Asn His Tyr Thr Thr Thr Arg Asp  
 180 185 190  
 Leu Ile Ser Ile Met Arg Cys Ala Leu Lys Glu Pro Pro Phe Arg Gly  
 195 200 205  
 Val Ile Ser Thr Thr Ser Tyr Lys Ile Gly Ala Thr Asn Leu His Gly  
 210 215 220  
 Glu Arg Ile Leu Ser Pro Thr Asn Lys Leu Leu Leu Pro Gly Ser Thr  
 225 230 235 240  
 60

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[illegible]

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Lys Lys Gln Ser Gly Tyr Arg Ser Pro Pro His Trp Leu Glu Thr Asp  
 60 65 70 75  
 Gly Ser Thr Ile Gln Leu His Leu Arg Glu Glu Leu Leu Gly Trp Asp  
 80 85 90  
 10 Leu Phe His Ala Leu Leu Val Cys Ser Ala Asn Asp Ala Ala Asn Val  
 95 100 105  
 Leu Ala Met Ala Cys Cys Gly Ser Val Glu Lys Phe Met Asp Lys Leu  
 110 115 120  
 Asn Phe Phe Leu Lys Glu Glu Ile Gly Cys Thr His Thr His Phe Asn  
 125 130 135  
 20 Asn Pro His Gly Leu His His Pro Asn His Tyr Thr Thr Thr Arg Asp  
 140 145 150 155  
 Leu Ile Ser Ile Met Arg Cys Ala Leu Lys Glu Pro Pro Phe Arg Gly  
 160 165 170  
 Val Ile Ser Thr Thr Ser Tyr Lys Ile Gly Ala Thr Asn Leu His Gly  
 175 180 185  
 Glu Arg Ile Leu Ser Pro Thr Asn Lys Leu Leu Leu Pro Gly Ser Thr  
 190 195 200  
 30 Tyr His Tyr Pro Pro Ala Leu Gly Gly Lys Thr Gly Thr Thr Lys Thr  
 205 210 215  
 Ala Gly Lys Asn Leu Ile Met Ala Ala Glu Lys Asn Asn Arg Leu Leu  
 220 225 230 235  
 Val Thr Ile Ala Thr Gly Tyr Ser Gly Pro  
 240 245  
 40 <210> 35  
 <211> 645  
 <212> PRT  
 <213> Chlamydia pneumoniae  
 <400> 35  
 Met Ala Ser Asn Pro Ile Leu Gln Ile Glu Asp Leu Ser Ile Thr Leu  
 1 5 10 15  
 50 Ala Lys Gln Arg Gln Gln Tyr Pro Ile Val Gln Ser Leu Ser Phe Thr  
 20 25 30  
 Ile Asn Glu Gly Gln Thr Leu Ala Ile Ile Gly Glu Ser Gly Ser Gly  
 35 40 45  
 Lys Ser Val Ser Ala His Ala Ile Leu Arg Leu Leu Pro Cys Pro Pro  
 50 55 60  
 Phe Ser Val Ser Gly Gln Val Asn Phe Gln Gly His Asn Leu Leu Thr  
 65 70 75 80  
 60

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	Ala	Ser	Arg	Ser	Ile	Gln	Lys	Lys	Ile	Ile	Gly	Thr	Glu	Ile	Ser	Met	
					85					90					95		
	Ile	Phe	Gln	Asn	Pro	Gln	Ala	Ser	Leu	Asn	Pro	Val	Phe	Thr	Ile	Glu	
				100					105					110			
10	Gln	Gln	Phe	Arg	Glu	Ile	Ile	His	Thr	His	Leu	Ala	Leu	Thr	Ala	Glu	
			115					120						125			
	Val	Ala	Lys	Glu	Lys	Met	Leu	Tyr	Ala	Leu	Glu	Glu	Thr	Gly	Phe	His	
		130					135						140				
	Asp	Pro	Arg	Leu	Cys	Leu	Asn	Leu	Tyr	Pro	His	Gln	Leu	Ser	Gly	Gly	
	145				150						155				160		
	Met	Leu	Gln	Arg	Ile	Cys	Ile	Ala	Met	Ala	Leu	Leu	Cys	Ser	Pro	Lys	
				165						170					175		
20	Leu	Leu	Ile	Ala	Asp	Glu	Pro	Thr	Thr	Ala	Leu	Asp	Val	Ser	Val	Gln	
				180					185					190			
	Tyr	Gln	Ile	Leu	Gln	Leu	Leu	Lys	Thr	Leu	Gln	Lys	Lys	Thr	Gly	Met	
			195					200					205				
	Ser	Leu	Leu	Ile	Ile	Thr	His	Asn	Met	Gly	Val	Val	Ala	Glu	Thr	Ala	
		210					215						220				
30	Asp	Asp	Val	Leu	Val	Leu	Tyr	Ala	Gly	Arg	Met	Val	Glu	Cys	Ala	Pro	
	225					230					235				240		
	Ala	Val	Gln	Met	Phe	His	Asn	Pro	Ser	His	Pro	Tyr	Thr	Arg	Asp	Leu	
				245						250					255		
	Leu	Ala	Ser	Arg	Pro	Ser	Leu	Gln	Pro	Gln	Gln	Leu	Gly	Ser	Phe	Asn	
				260					265					270			
40	Pro	Ile	Pro	Gly	Gln	Pro	Pro	His	Tyr	Thr	Ala	Phe	Pro	Ser	Gly	Cys	
		275						280					285				
	Arg	Tyr	His	Pro	Arg	Cys	Ser	Lys	Ile	Leu	Asn	Arg	Cys	Ser	Ala	Glu	
		290					295					300					
	Ala	Pro	Glu	Ile	Tyr	Pro	Val	Arg	Glu	Gly	His	Lys	Val	Arg	Val	Gly	
	305				310						315				320		
	Cys	Met	Thr	Thr	Asn	Phe	Pro	Gln	Pro	Leu	Ile	Gln	Ala	Thr	Ser	Leu	
				325						330					335		
50	Thr	Lys	His	Tyr	Tyr	Lys	Arg	Ser	Phe	Trp	Phe	Gln	Gly	Lys	Thr	Ile	
				340					345					350			
	Ala	Ser	Arg	Pro	Val	Asp	Asp	Val	Ser	Phe	Ser	Leu	Tyr	Ser	Arg	Arg	
			355					360					365				
	Ala	Val	Gly	Leu	Ile	Gly	Glu	Ser	Gly	Ser	Gly	Lys	Ser	Thr	Leu	Ala	
		370					375					380					
60	Leu	Ala	Leu	Ala	Gly	Leu	Leu	Pro	Leu	Thr	Ser	Gly	Phe	Leu	Thr	Phe	
	385					390					395					400	



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Asn Gly Thr Pro Ile Lys Leu His Ser Lys His Gly Arg His Gln Leu  
 405 410 415  
 Arg Ser Gln Val Arg Leu Val Phe Gln Asn Pro Gln Ala Ser Leu Asn  
 420 425 430  
 10 Pro Arg Lys Thr Ile Leu Asp Ser Leu Gly His Ser Leu Leu Tyr His  
 435 440 445  
 Lys Leu Val Pro Lys Glu Lys Val Leu Ala Thr Val Arg Glu Tyr Leu  
 450 455 460  
 Glu Leu Val Gly Leu Ser Glu Glu Tyr Phe Tyr Arg Tyr Pro His Gln  
 465 470 475 480  
 Leu Ser Gly Gly Gln Gln Arg Val Ser Ile Ala Arg Ala Leu Leu  
 485 490 495  
 20 Gly Val Pro Gln Leu Ile Ile Cys Asp Glu Ile Val Ser Ala Leu Asp  
 500 505 510  
 Leu Ser Ile Gln Ala Gln Ile Leu Asn Met Leu Ala Glu Leu Gln Lys  
 515 520 525  
 Lys Leu Ser Leu Thr Tyr Leu Phe Ile Ser His Asp Leu Ala Val Val  
 530 535 540  
 30 Arg Ser Phe Cys Thr Glu Val Phe Ile Met Tyr Lys Gly Gln Ile Val  
 545 550 555 560  
 Glu Lys Gly Asn Thr Lys Arg Ile Phe Ser Asp Pro Gln His Pro Tyr  
 565 570 575  
 Thr Arg Met Leu Leu Asn Ala Gln Leu Pro Glu Thr Pro Asp Gln Arg  
 580 585 590  
 40 Gln Ser Lys Pro Ile Phe Gln Glu Tyr His Lys Asp Ser Glu Glu Ser  
 595 600 605  
 Cys Ser Thr Gly Cys Tyr Phe Tyr Asn Arg Cys Pro Gln Lys Gln Glu  
 610 615 620  
 Ala Cys Lys Ser Glu Ile Ile Pro Asn Gln Gly Asp Ala His His Thr  
 625 630 635 640  
 Tyr Arg Cys Ile His  
 645  
 50  
 <210> 36  
 <211> 588  
 <212> PRT  
 <213> Chlamydia pneumoniae  
 <400> 36  
 Ile Leu Gln Ile Glu Asp Leu Ser Ile Thr Leu  
 1 5 10

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	Ala	Lys	Gln	Arg	Gln	Gln	Tyr	Pro	Ile	Val	Gln	Ser	Leu	Ser	Phe	Thr	
				15					20					25			
	Ile	Asn	Glu	Gly	Gln	Thr	Leu	Ala	Ile	Ile	Gly	Glu	Ser	Gly	Ser	Gly	
			30					35					40				
10	Lys	Ser	Val	Ser	Ala	His	Ala	Ile	Leu	Arg	Leu	Leu	Pro	Cys	Pro	Pro	
		45					50					55					
	Phe	Ser	Val	Ser	Gly	Gln	Val	Asn	Phe	Gln	Gly	His	Asn	Leu	Leu	Thr	
		60				65					70					75	
	Ala	Ser	Arg	Ser	Ile	Gln	Lys	Lys	Ile	Ile	Gly	Thr	Glu	Ile	Ser	Met	
					80					85					90		
	Ile	Phe	Gln	Asn	Pro	Gln	Ala	Ser	Leu	Asn	Pro	Val	Phe	Thr	Ile	Glu	
20				95					100					105			
	Gln	Gln	Phe	Arg	Glu	Ile	Ile	His	Thr	His	Leu	Ala	Leu	Thr	Ala	Glu	
				110					115					120			
	Val	Ala	Lys	Glu	Lys	Met	Leu	Tyr	Ala	Leu	Glu	Glu	Thr	Gly	Phe	His	
		125					130					135					
	Asp	Pro	Arg	Leu	Cys	Leu	Asn	Leu	Tyr	Pro	His	Gln	Leu	Ser	Gly	Gly	
		140				145					150					155	
30	Met	Leu	Gln	Arg	Ile	Cys	Ile	Ala	Met	Ala	Leu	Leu	Cys	Ser	Pro	Lys	
				160						165					170		
	Leu	Leu	Ile	Ala	Asp	Glu	Pro	Thr	Thr	Ala	Leu	Asp	Val	Ser	Val	Gln	
				175					180					185			
	Tyr	Gln	Ile	Leu	Gln	Leu	Leu	Lys	Thr	Leu	Gln	Lys	Lys	Thr	Gly	Met	
			190					195					200				
40	Ser	Leu	Leu	Ile	Ile	Thr	His	Asn	Met	Gly	Val	Val	Ala	Glu	Thr	Ala	
		205					210					215					
	Asp	Asp	Val	Leu	Val	Leu	Tyr	Ala	Gly	Arg	Met	Val	Glu	Cys	Ala	Pro	
		220				225					230					235	
	Ala	Val	Gln	Met	Phe	His	Asn	Pro	Ser	His	Pro	Tyr	Thr	Arg	Asp	Leu	
				240						245					250		
	Leu	Ala	Ser	Arg	Pro	Ser	Leu	Gln	Pro	Gln	Gln	Leu	Gly	Ser	Phe	Asn	
50				255					260					265			
	Pro	Ile	Pro	Gly	Gln	Pro	Pro	His	Tyr	Thr	Ala	Phe	Pro	Ser	Gly	Cys	
			270					275					280				
	Arg	Tyr	His	Pro	Arg	Cys	Ser	Lys	Ile	Leu	Asn	Arg	Cys	Ser	Ala	Glu	
		285					290					295					
	Ala	Pro	Glu	Ile	Tyr	Pro	Val	Arg	Glu	Gly	His	Lys	Val	Arg	Val	Gly	
		300				305					310					315	
60	Cys	Met	Thr	Thr	Asn	Phe	Pro	Gln	Pro	Leu	Ile	Gln	Ala	Thr	Ser	Leu	
					320					325					330		

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	Thr	Lys	His	Tyr	Thr	Lys	Arg	Ser	Phe	Trp	Phe	Gln	Gly	Lys	Thr	Ile
	335										340			345		
	Ala	Ser	Arg	Pro	Val	Asp	Asp	Val	Ser	Phe	Ser	Leu	Tyr	Ser	Arg	Arg
	350										355			360		
10	Ala	Val	Gly	Leu	Ile	Gly	Glu	Ser	Gly	Ser	Gly	Lys	Ser	Thr	Leu	Ala
	365										370			375		
	Leu	Ala	Leu	Ala	Gly	Leu	Leu	Pro	Leu	Thr	Ser	Gly	Phe	Leu	Thr	Phe
	380										385			390		
	Asn	Gly	Thr	Pro	Ile	Lys	Leu	His	Ser	Lys	His	Gly	Arg	His	Gln	Leu
	400										405			410		
20	Arg	Ser	Gln	Val	Arg	Leu	Val	Phe	Gln	Asn	Pro	Gln	Ala	Ser	Leu	Asn
	415										420			425		
	Pro	Arg	Lys	Thr	Ile	Leu	Asp	Ser	Leu	Gly	His	Ser	Leu	Leu	Tyr	His
	430										435			440		
	Lys	Leu	Val	Pro	Lys	Glu	Lys	Val	Leu	Ala	Thr	Val	Arg	Glu	Tyr	Leu
	445										450			455		
	Glu	Leu	Val	Gly	Leu	Ser	Glu	Glu	Tyr	Phe	Tyr	Arg	Tyr	Pro	His	Gln
	460										465			470		
30	Leu	Ser	Gly	Gly	Gln	Gln	Gln	Arg	Val	Ser	Ile	Ala	Arg	Ala	Leu	Leu
	480										485			490		
	Gly	Val	Pro	Gln	Leu	Ile	Ile	Cys	Asp	Glu	Ile	Val	Ser	Ala	Leu	Asp
	495										500			505		
	Leu	Ser	Ile	Gln	Ala	Gln	Ile	Leu	Asn	Met	Leu	Ala	Glu	Leu	Gln	Lys
	510										515			520		
40	Lys	Leu	Ser	Leu	Thr	Tyr	Leu	Phe	Ile	Ser	His	Asp	Leu	Ala	Val	Val
	525										530			535		
	Arg	Ser	Phe	Cys	Thr	Glu	Val	Phe	Ile	Met	Tyr	Lys	Gly	Gln	Ile	Val
	540										545			550		
	Glu	Lys	Gly	Asn	Thr	Lys	Arg	Ile	Phe	Ser	Asp	Pro	Gln	His	Pro	Tyr
	560										565			570		
50	Thr	Arg	Met	Leu	Leu	Asn	Ala	Gln	Leu	Pro	Glu	Thr	Pro	Asp	Gln	Arg
	575										585			585		
	Gln															
	<210> 37															
	<211> 698															
	<212> PRT															
	<213> Chlamydia pneumoniae .															
	<400> 37															
60	Met	Pro	Gly	Ile	Glu	Lys	Ala	Ala	Thr	Thr	Val	Ala	Val	Pro	Gln	Asp
	1 5 10 15															

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Lys Ser Glu Glu Glu Lys Val Lys Glu Arg Leu Thr Lys Arg Glu Leu  
 20 25 30  
 Thr Cys Glu Asp Leu Lys Asp Asn Gly Tyr Thr Val Asn Phe Glu Asp  
 35 40 45  
 10 Ile Ser Ile Leu Glu Leu Leu Gln Phe Val Ser Lys Ile Ser Gly Thr  
 50 55 60  
 Asn Phe Val Phe Asp Ser Asn Asp Leu Gln Phe Asn Val Thr Ile Val  
 65 70 75 80  
 Ser His Asp Pro Thr Ser Val Asp Asp Leu Ser Thr Ile Leu Leu Gln  
 85 90 95  
 20 Val Leu Lys Met His Asp Leu Lys Val Val Glu Gln Gly Asn Asn Val  
 100 105 110  
 Leu Ile Tyr Arg Asn Pro His Leu Ser Lys Leu Ser Thr Val Val Thr  
 115 120 125  
 Asp Ser Ser Leu Lys Glu Thr Cys Glu Ala Val Val Thr Arg Val  
 130 135 140  
 Phe Arg Leu Tyr Arg Arg Gln Pro Ser Ala Ala Val Asn Ile Ile Gln  
 145 150 155 160  
 30 Pro Leu Leu Ser His Asp Ala Ile Val Ser Ala Ser Glu Ala Thr Arg  
 165 170 175  
 His Val Ile Ile Ser Asp Ile Ala Gly Asn Val Asp Lys Val Ser Asp  
 180 185 190  
 Leu Leu Ala Ala Leu Asp Cys Pro Gly Thr Ser Val Asp Met Thr Glu  
 195 200 205  
 40 Tyr Glu Val Lys Tyr Ala Asn Pro Ala Ala Leu Val Ser Tyr Cys Gln  
 210 215 220  
 Asp Val Leu Gly Thr Leu Ala Glu Asp Asp Ala Phe Gln Met Phe Ile  
 225 230 235 240  
 Gln Pro Gly Thr Asn Lys Ile Phe Val Val Ser Ser Pro Arg Leu Ala  
 245 250 255  
 Asn Lys Ala Glu Gln Leu Leu Lys Ser Leu Asp Val Pro Glu Met Ala  
 260 265 270  
 50 His Thr Leu Asp Asp Pro Ala Ser Thr Ala Leu Ala Leu Gly Gly Thr  
 275 280 285  
 Gly Thr Thr Ser Pro Lys Ser Leu Arg Phe Phe Met Tyr Lys Leu Lys  
 290 295 300  
 Tyr Gln Asn Gly Glu Val Ile Ala Asn Ala Leu Gln Asp Ile Gly Tyr  
 305 310 315 320  
 60 Asn Leu Tyr Val Thr Thr Ala Met Asp Glu Asp Phe Ile Asn Thr Leu  
 325 330 335

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Asn Ser Ile Gln Trp Leu Glu Val Asn Asn Ser Ile Val Ile Ile Gly  
 340 345 350  
 Asn Gln Gly Asn Val Asp Arg Val Ile Gly Leu Leu Asn Gly Leu Asp  
 355 360 365  
 10 Leu Pro Pro Lys Gln Val Tyr Ile Glu Val Leu Ile Leu Asp Thr Ser  
 370 375 380  
 Leu Glu Lys Ser Trp Asp Phe Gly Val Gln Trp Val Ala Leu Gly Asp  
 385 390 395 400  
 Glu Gln Ser Lys Val Ala Tyr Ala Ser Gly Leu Leu Asn Asn Thr Gly  
 405 410 415  
 Ile Ala Thr Pro Thr Lys Ala Thr Val Pro Pro Gly Thr Pro Asn Pro  
 420 425 430  
 20 Gly Ser Ile Pro Leu Pro Thr Pro Gly Gln Leu Thr Gly Phe Ser Asp  
 435 440 445  
 Met Leu Asn Ser Ser Ser Ala Phe Gly Leu Gly Ile Ile Gly Asn Val  
 450 455 460  
 Leu Ser His Lys Gly Lys Ser Phe Leu Thr Leu Gly Gly Leu Leu Ser  
 465 470 475 480  
 30 Ala Leu Asp Gln Asp Gly Asp Thr Val Ile Val Leu Asn Pro Arg Ile  
 485 490 495  
 Met Ala Gln Asp Thr Gln Gln Ala Ser Phe Phe Val Gly Gln Thr Val  
 500 505 510  
 Pro Tyr Gln Thr Ile Lys Tyr Tyr Ile Gln Glu Thr Gly Thr Val Thr  
 515 520 525  
 40 Gln Asn Ile Asp Tyr Glu Asp Ile Gly Val Asn Leu Val Val Thr Ser  
 530 535 540  
 Thr Val Ala Pro Asn Asn Val Val Thr Leu Gln Ile Glu Gln Thr Ile  
 545 550 555 560  
 Ser Glu Leu His Ser Ala Ser Gly Ser Leu Thr Pro Val Thr Asp Lys  
 565 570 575  
 Thr Tyr Ala Ala Thr Arg Leu Gln Ile Pro Asp Gly Cys Phe Leu Val  
 580 585 590  
 50 Met Ser Gly His Ile Arg Asp Lys Thr Thr Lys Val Val Ser Gly Val  
 595 600 605  
 Pro Leu Leu Asn Ser Ile Pro Leu Ile Arg Gly Leu Phe Ser Arg Thr  
 610 615 620  
 Ile Asp Gln Arg Gln Lys Arg Asn Ile Met Met Phe Ile Lys Pro Lys  
 625 630 635 640  
 60 Val Ile Ser Ser Phe Glu Glu Gly Thr Arg Val Thr Asn Lys Glu Gly  
 645 650 655

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Tyr Arg Tyr Asn Trp Glu Ala Asp Glu Gly Ser Met Gln Val Ala Pro  
 660 665 670  
 Arg His Ala Pro Glu Cys Gln Gly Pro Pro Ser Leu Gln Ala Glu Ser  
 675 680 685  
 Asp Phe Lys Ile Ile Glu Ile Glu Ala Gln  
 690 695  
 <210> 38  
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 <212> PRT  
 <213> Chlamydia pneumoniae  
 <400> 38  
 Met Ser Arg Lys Asp Asn Glu Val Ser Leu Ala Arg Ser Ile Phe Asn  
 1 5 10 15  
 Ile Leu Ser Gly Thr Phe Cys Ser Arg Ile Thr Gly Ile Phe Arg Glu  
 20 25 30  
 Ile Ala Met Ala Thr Tyr Phe Gly Ala Asp Pro Ile Val Ala Ala Phe  
 35 40 45  
 Trp Leu Gly Phe Arg Thr Val Phe Phe Leu Arg Lys Ile Leu Gly Gly  
 50 55 60  
 Leu Ile Leu Glu Gln Ala Phe Ile Pro His Phe Glu Phe Leu Arg Ala  
 65 70 75 80  
 Gln Ser Leu Asp Arg Ala Ala Phe Phe Phe Arg Arg Phe Ser Arg Leu  
 85 90 95  
 Ile Lys Gly Ser Thr Ile Ile Phe Thr Leu Leu Ile Glu Ala Val Leu  
 100 105 110  
 Trp Val Phe Phe Asn Asn Val Glu Glu Gly Thr Tyr Asp Met Ile Leu  
 115 120 125  
 Leu Thr Met Ile Leu Leu Pro Cys Gly Ile Phe Leu Met Met Tyr Asn  
 130 135 140  
 Val Asn Gly Ala Leu Leu His Cys Gly Asn Lys Phe Phe Gly Val Gly  
 145 150 155 160  
 Leu Ala Pro Val Val Val Asn Ile Ile Trp Ile Phe Phe Val Ile Ala  
 165 170 175  
 Ala Arg His Ser Asp Pro Arg Glu Arg Ile Ile Gly Leu Ser Val Ala  
 180 185 190  
 Leu Val Ile Gly Phe Phe Phe Glu Trp Leu Ile Thr Val Pro Gly Val  
 195 200 205  
 Trp Lys Phe Leu Leu Glu Ala Lys Ser Pro Pro Gln Glu His Asp Ser  
 210 215 220  
 60

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Val Arg Ala Leu Leu Ala Pro Leu Ser Leu Gly Ile Leu Thr Ser Ser  
 225 230 235 240  
 Ile Phe Gln Leu Asn Leu Leu Ser Asp Ile Cys Leu Ala Arg Tyr Val  
 245 250 255  
 10 His Glu Ile Gly Pro Leu Tyr Leu Met Tyr Ser Leu Lys Ile Tyr Gln  
 260 265 270  
 Leu Pro Ile His Leu Phe Gly Phe Gly Val Phe Thr Val Leu Leu Pro  
 275 280 285  
 Ala Ile Ser Arg Cys Val Gln Arg Glu Asp His Glu Arg Gly Leu Lys  
 290 295 300  
 20 Leu Met Lys Phe Val Leu Thr Leu Thr Met Ser Val Met Ile Ile Met  
 305 310 315 320  
 Thr Ala Gly Leu Leu Leu Leu Ala Leu Pro Gly Val Arg Val Leu Tyr  
 325 330 335  
 Glu His Gly Leu Phe Pro Gln Ser Ala Val Tyr Ala Ile Val Arg Val  
 340 345 350  
 Leu Arg Gly Tyr Gly Ala Ser Ile Ile Pro Met Ala Leu Ala Pro Leu  
 355 360 365  
 30 Val Ser Val Leu Phe Tyr Ala Gln Arg Gln Tyr Ala Val Pro Leu Phe  
 370 375 380  
 Ile Gly Ile Gly Thr Ala Leu Ala Asn Ile Val Leu Ser Leu Val Leu  
 385 390 395 400  
 Gly Arg Trp Val Leu Lys Asp Val Ser Gly Ile Ser Tyr Ala Thr Ser  
 405 410 415  
 40 Ile Thr Ala Trp Val Gln Leu Tyr Phe Leu Trp Tyr Tyr Ser Ser Lys  
 420 425 430  
 Arg Leu Pro Met Tyr Ser Lys Leu Leu Trp Glu Ser Ile Arg Arg Ser  
 435 440 445  
 Ile Lys Val Met Gly Thr Thr Met Leu Ala Cys Met Ile Thr Leu Gly  
 450 455 460  
 50 Leu Asn Ile Leu Thr Gln Thr Thr Tyr Val Ile Phe Leu Asn Pro Leu  
 465 470 475 480  
 Thr Pro Leu Ala Trp Pro Leu Ser Ser Ile Thr Ala Gln Ala Ile Ala  
 485 490 495  
 Phe Leu Ser Glu Ser Cys Ile Phe Leu Ala Phe Leu Phe Gly Phe Ala  
 500 505 510  
 Lys Leu Leu Arg Val Glu Asp Leu Ile Asn Leu Ala Ser Phe Glu Tyr  
 515 520 525  
 60 Trp Arg Gly Gln Arg Gly Leu Leu Gln Arg Gln His Val Met Gln Asp  
 530 535 540

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Thr Gln Asn  
545

<210> 39  
<211> 535  
<212> PRT

10 <213> Chlamydia pneumoniae

<400> 39

Arg Lys Asp Asn Glu Val Ser Leu Ala Arg Ser Ile Phe Asn  
1 5 10

Ile Leu Ser Gly Thr Phe Cys Ser Arg Ile Thr Gly Ile Phe Arg Glu  
15 20 25 30

20 Ile Ala Met Ala Thr Tyr Phe Gly Ala Asp Pro Ile Val Ala Ala Phe  
35 40 45

Trp Leu Gly Phe Arg Thr Val Phe Phe Leu Arg Lys Ile Leu Gly Gly  
50 55 60

Leu Ile Leu Glu Gln Ala Phe Ile Pro His Phe Glu Phe Leu Arg Ala  
65 70 75

Gln Ser Leu Asp Arg Ala Ala Phe Phe Phe Arg Arg Phe Ser Arg Leu  
80 85 90

30 Ile Lys Gly Ser Thr Ile Ile Phe Thr Leu Leu Ile Glu Ala Val Leu  
95 100 105 110

Trp Val Phe Phe Asn Asn Val Glu Glu Gly Thr Tyr Asp Met Ile Leu  
115 120 125

Leu Thr Met Ile Leu Leu Pro Cys Gly Ile Phe Leu Met Met Tyr Asn  
130 135 140

40 Val Asn Gly Ala Leu Leu His Cys Gly Asn Lys Phe Phe Gly Val Gly  
145 150 155

Leu Ala Pro Val Val Val Asn Ile Ile Trp Ile Phe Phe Val Ile Ala  
160 165 170

Ala Arg His Ser Asp Pro Arg Glu Arg Ile Ile Gly Leu Ser Val Ala  
175 180 185 190

50 Leu Val Ile Gly Phe Phe Phe Glu Trp Leu Ile Thr Val Pro Gly Val  
195 200 205

Trp Lys Phe Leu Leu Glu Ala Lys Ser Pro Pro Gln Glu His Asp Ser  
210 215 220

Val Arg Ala Leu Leu Ala Pro Leu Ser Leu Gly Ile Leu Thr Ser Ser  
225 230 235

Ile Phe Gln Leu Asn Leu Leu Ser Asp Ile Cys Leu Ala Arg Tyr Val  
240 245 250

60



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His Glu Ile Gly Pro Leu Tyr Leu Met Tyr Ser Leu Lys Ile Tyr Gln  
 255 260 265 270  
 Leu Pro Ile His Leu Phe Gly Phe Gly Val Phe Thr Val Leu Leu Pro  
 275 280 285  
 10 Ala Ile Ser Arg Cys Val Gln Arg Glu Asp His Glu Arg Gly Leu Lys  
 290 295 300  
 Leu Met Lys Phe Val Leu Thr Leu Thr Met Ser Val Met Ile Ile Met  
 305 310 315  
 Thr Ala Gly Leu Leu Leu Leu Ala Leu Pro Gly Val Arg Val Leu Tyr  
 320 325 330  
 20 Glu His Gly Leu Phe Pro Gln Ser Ala Val Tyr Ala Ile Val Arg Val  
 335 340 345 350  
 Leu Arg Gly Tyr Gly Ala Ser Ile Ile Pro Met Ala Leu Ala Pro Leu  
 355 360 365  
 Val Ser Val Leu Phe Tyr Ala Gln Arg Gln Tyr Ala Val Pro Leu Phe  
 370 375 380  
 Ile Gly Ile Gly Thr Ala Leu Ala Asn Ile Val Leu Ser Leu Val Leu  
 385 390 395  
 30 Gly Arg Trp Val Leu Lys Asp Val Ser Gly Ile Ser Tyr Ala Thr Ser  
 400 405 410  
 Ile Thr Ala Trp Val Gln Leu Tyr Phe Leu Trp Tyr Tyr Ser Ser Lys  
 415 420 425 430  
 Arg Leu Pro Met Tyr Ser Lys Leu Leu Trp Glu Ser Ile Arg Arg Ser  
 435 440 445  
 40 Ile Lys Val Met Gly Thr Thr Met Leu Ala Cys Met Ile Thr Leu Gly  
 450 455 460  
 Leu Asn Ile Leu Thr Gln Thr Thr Tyr Val Ile Phe Leu Asn Pro Leu  
 465 470 475  
 Thr Pro Leu Ala Trp Pro Leu Ser Ser Ile Thr Ala Gln Ala Ile Ala  
 480 485 490  
 50 Phe Leu Ser Glu Ser Cys Ile Phe Leu Ala Phe Leu Phe Gly Phe Ala  
 495 500 505 510  
 Lys Leu Leu Arg Val Glu Asp Leu Ile Asn Leu Ala Ser Phe Glu Tyr  
 515 520 525  
 Trp Arg Gly Gln Arg Gly Leu Leu Gln  
 530 535  
 <210> 40  
 <211> 954  
 60 <212> PRT  
 <213> Chlamydia pneumoniae

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<400> 40  
 Met Lys Thr Ser Arg Asn Lys Gln Cys Lys Ile Thr Asp Pro Leu Ser  
 1 5 10 15  
 Lys Ser Ser Phe Phe Val Gly Ala Leu Ile Leu Gly Lys Thr Thr Ile  
 20 25 30  
 10 Leu Leu Asn Ala Thr Pro Leu Ser Asp Tyr Phe Asp Asn Gln Ala Asn  
 35 40 45  
 Gln Leu Thr Thr Leu Phe Pro Leu Ile Asp Thr Leu Thr Asn Met Thr  
 50 55 60  
 Pro Tyr Ser His Arg Ala Thr Leu Phe Gly Val Arg Asp Asp Thr Asn  
 65 70 75 80  
 20 Gln Asp Ile Val Leu Asp His Gln Asn Ser Ile Glu Ser Trp Phe Glu  
 85 90 95  
 Asn Phe Ser Gln Asp Gly Gly Ala Leu Ser Cys Lys Ser Leu Ala Ile  
 100 105 110  
 Thr Asn Thr Lys Asn Gln Ile Leu Phe Leu Asn Ser Phe Ala Ile Lys  
 115 120 125  
 Arg Ala Gly Ala Met Tyr Val Asp Gly Asn Phe Asp Leu Ser Glu Asn  
 130 135 140  
 30 His Gly Ser Ile Ile Phe Ser Gly Asn Leu Ser Phe Pro Asn Ala Ser  
 145 150 155 160  
 Asn Phe Ala Asp Thr Cys Thr Gly Gly Ala Val Leu Cys Ser Lys Asn  
 165 170 175  
 Val Thr Ile Ser Lys Asn Gln Gly Thr Ala Tyr Phe Ile Asn Asn Lys  
 180 185 190  
 40 Ala Lys Ser Ser Gly Gly Ala Ile Gln Ala Ala Ile Ile Asn Ile Lys  
 195 200 205  
 Asp Asn Thr Gly Pro Cys Leu Phe Phe Asn Asn Ala Ala Gly Gly Thr  
 210 215 220  
 Ala Gly Gly Ala Leu Phe Ala Asn Ala Cys Arg Ile Glu Asn Asn Ser  
 225 230 235 240  
 50 Gln Pro Ile Tyr Phe Leu Asn Asn Gln Ser Gly Leu Gly Gly Ala Ile  
 245 250 255  
 Arg Val His Gln Glu Cys Ile Leu Thr Lys Asn Thr Gly Ser Val Ile  
 260 265 270  
 Phe Asn Asn Asn Phe Ala Met Glu Ala Asp Ile Ser Ala Asn His Ser  
 275 280 285  
 Ser Gly Gly Ala Ile Tyr Cys Ile Ser Cys Ser Ile Lys Asp Asn Pro  
 290 295 300  
 60

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Gly Ile Ala Ala Phe Asp Asn Asn Thr Ala Ala Arg Asp Gly Gly Ala  
 305 310 315 320  
 Ile Cys Thr Gln Ser Leu Thr Ile Gln Asp Ser Gly Pro Val Tyr Phe  
 325 330 335  
 10 Thr Asn Asn Gln Gly Thr Trp Gly Gly Ala Ile Met Leu Arg Gln Asp  
 340 345 350  
 Gly Ala Cys Thr Leu Phe Ala Asp Gln Gly Asp Ile Ile Phe Tyr Asn  
 355 360 365  
 Asn Arg His Phe Lys Asp Thr Phe Ser Asn His Val Ser Val Asn Cys  
 370 375 380  
 20 Thr Arg Asn Val Ser Leu Thr Val Gly Ala Ser Gln Gly His Ser Ala  
 385 390 395 400  
 Thr Phe Tyr Asp Pro Ile Leu Gln Arg Tyr Thr Ile Gln Asn Ser Ile  
 405 410 415  
 Gln Lys Phe Asn Pro Asn Pro Glu His Leu Gly Thr Ile Leu Phe Ser  
 420 425 430  
 Ser Thr Tyr Ile Pro Asp Thr Ser Thr Ser Arg Asp Asp Phe Ile Ser  
 435 440 445  
 30 His Phe Arg Asn His Ile Gly Leu Tyr Asn Gly Thr Leu Ala Leu Glu  
 450 455 460  
 Asp Arg Ala Glu Trp Lys Val Tyr Lys Phe Asp Gln Phe Gly Gly Thr  
 465 470 475 480  
 Leu Arg Leu Gly Ser Arg Ala Val Phe Ser Thr Thr Asp Glu Glu Gln  
 485 490 495  
 40 Ser Ser Ser Ser Val Gly Ser Val Ile Asn Ile Asn Asn Leu Ala Ile  
 500 505 510  
 Asn Leu Pro Ser Ile Leu Gly Asn Arg Val Ala Pro Lys Leu Trp Ile  
 515 520 525  
 Arg Pro Thr Gly Ser Ser Ala Pro Tyr Ser Glu Asp Asn Asn Pro Ile  
 530 535 540  
 50 Ile Asn Leu Ser Gly Pro Leu Ser Leu Leu Asp Asp Glu Asn Leu Asp  
 545 550 555 560  
 Pro Tyr Asp Thr Ala Asp Leu Ala Gln Pro Ile Ala Glu Val Pro Leu  
 565 570 575  
 Leu Tyr Leu Leu Asp Val Thr Ala Lys His Ile Asn Thr Asp Asn Phe  
 580 585 590  
 Tyr Pro Glu Gly Leu Asn Thr Thr Gln His Tyr Gly Tyr Gln Gly Val  
 595 600 605  
 60 Trp Ser Pro Tyr Trp Ile Glu Thr Ile Thr Thr Ser Asp Thr Ser Ser  
 610 615 620

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	Glu	Asp	Thr	Val	Asn	Thr	Leu	His	Arg	Gln	Leu	Tyr	Gly	Asp	Trp	Thr	
	625					630					635					640	
	Pro	Thr	Gly	Tyr	Lys	Val	Asn	Pro	Glu	Asn	Lys	Gly	Asp	Ile	Ala	Leu	
					645					650					655		
10	Ser	Ala	Phe	Trp	Gln	Ser	Phe	His	Asn	Leu	Phe	Ala	Thr	Leu	Arg	Tyr	
				660					665					670			
	Gln	Thr	Gln	Gln	Gly	Gln	Ile	Ala	Pro	Thr	Ala	Ser	Gly	Glu	Ala	Thr	
								680					685				
	Arg	Leu	Phe	Val	His	Gln	Asn	Ser	Asn	Asn	Asp	Ala	Lys	Gly	Phe	His	
		690					695					700					
20	Met	Glu	Ala	Thr	Gly	Tyr	Ser	Leu	Gly	Thr	Thr	Ser	Asn	Thr	Ala	Ser	
	705					710					715					720	
	Asn	His	Ser	Phe	Gly	Val	Asn	Phe	Ser	Gln	Leu	Phe	Ser	Asn	Leu	Tyr	
					725					730					735		
	Glu	Ser	His	Ser	Asp	Asn	Ser	Val	Ala	Ser	His	Thr	Thr	Thr	Val	Ala	
				740					745						750		
	Leu	Gln	Ile	Asn	Asn	Pro	Trp	Leu	Gln	Glu	Arg	Phe	Ser	Thr	Ser	Ala	
			755					760					765				
30	Ser	Leu	Ala	Tyr	Ser	Tyr	Ser	Asn	His	His	Ile	Lys	Ala	Ser	Gly	Tyr	
		770					775					780					
	Ser	Gly	Lys	Ile	Gln	Thr	Glu	Gly	Lys	Cys	Tyr	Ser	Thr	Thr	Leu	Gly	
	785					790					795					800	
	Ala	Ala	Leu	Ser	Cys	Ser	Leu	Ser	Leu	Gln	Trp	Arg	Ser	Arg	Pro	Leu	
				805						810					815		
40	His	Phe	Thr	Pro	Phe	Ile	Gln	Ala	Ile	Ala	Val	Arg	Ser	Asn	Gln	Thr	
				820					825					830			
	Ala	Phe	Gln	Glu	Ser	Gly	Asp	Lys	Ala	Arg	Lys	Phe	Ser	Val	His	Lys	
			835					840					845				
	Pro	Leu	Tyr	Asn	Leu	Thr	Val	Pro	Leu	Gly	Ile	Gln	Ser	Ala	Trp	Glu	
		850					855					860					
50	Ser	Lys	Phe	Arg	Leu	Pro	Thr	Tyr	Trp	Asn	Ile	Glu	Leu	Ala	Tyr	Gln	
	865					870					875					880	
	Pro	Val	Leu	Tyr	Gln	Gln	Asn	Pro	Glu	Ile	Asn	Val	Ser	Leu	Glu	Ser	
					885					890					895		
	Ser	Gly	Ser	Ser	Trp	Leu	Leu	Ser	Gly	Thr	Thr	Leu	Ala	Arg	Asn	Ala	
				900					905					910			
	Ile	Ala	Phe	Lys	Gly	Arg	Asn	Gln	Ile	Phe	Ile	Phe	Pro	Lys	Leu	Ser	
			915					920					925				
60	Val	Phe	Leu	Asp	Tyr	Gln	Gly	Ser	Val	Ser	Ser	Ser	Thr	Thr	Thr	His	
		930					935						940				

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Tyr Leu His Ala Gly Thr Thr Phe Lys Phe  
945 950

<210> 41

<211> 788

<212> PRT

10 <213> Chlamydia pneumoniae

<400> 41

Thr Gly Gly Ala Val Leu Cys Ser Lys Asn  
1 5 10

Val Thr Ile Ser Lys Asn Gln Gly Thr Ala Tyr Phe Ile Asn Asn Lys  
15 20 25

20 Ala Lys Ser Ser Gly Gly Ala Ile Gln Ala Ala Ile Ile Asn Ile Lys  
30 35 40

Asp Asn Thr Gly Pro Cys Leu Phe Asn Asn Ala Ala Gly Gly Thr  
45 50 55

Ala Gly Gly Ala Leu Phe Ala Asn Ala Cys Arg Ile Glu Asn Asn Ser  
60 65 70

30 Gln Pro Ile Tyr Phe Leu Asn Asn Gln Ser Gly Leu Gly Gly Ala Ile  
75 80 85 90

Arg Val His Gln Glu Cys Ile Leu Thr Lys Asn Thr Gly Ser Val Ile  
95 100 105

Phe Asn Asn Asn Phe Ala Met Glu Ala Asp Ile Ser Ala Asn His Ser  
110 115 120

Ser Gly Gly Ala Ile Tyr Cys Ile Ser Cys Ser Ile Lys Asp Asn Pro  
125 130 135

40 Gly Ile Ala Ala Phe Asp Asn Asn Thr Ala Ala Arg Asp Gly Gly Ala  
140 145 150

Ile Cys Thr Gln Ser Leu Thr Ile Gln Asp Ser Gly Pro Val Tyr Phe  
155 160 165 170

Thr Asn Asn Gln Gly Thr Trp Gly Gly Ala Ile Met Leu Arg Gln Asp  
175 180 185

50 Gly Ala Cys Thr Leu Phe Ala Asp Gln Gly Asp Ile Ile Phe Tyr Asn  
190 195 200

Asn Arg His Phe Lys Asp Thr Phe Ser Asn His Val Ser Val Asn Cys  
205 210 215

Thr Arg Asn Val Ser Leu Thr Val Gly Ala Ser Gln Gly His Ser Ala  
220 225 230

Thr Phe Tyr Asp Pro Ile Leu Gln Arg Tyr Thr Ile Gln Asn Ser Ile  
235 240 245 250

60

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	Gln	Lys	Phe	Asn	Pro	Asn	Pro	Glu	His	Leu	Gly	Thr	Ile	Leu	Phe	Ser
					255					260					265	
	Ser	Thr	Tyr	Ile	Pro	Asp	Thr	Ser	Thr	Ser	Arg	Asp	Asp	Phe	Ile	Ser
				270					275					280		
10	His	Phe	Arg	Asn	His	Ile	Gly	Leu	Tyr	Asn	Gly	Thr	Leu	Ala	Leu	Glu
			285					290					295			
	Asp	Arg	Ala	Glu	Trp	Lys	Val	Tyr	Lys	Phe	Asp	Gln	Phe	Gly	Gly	Thr
		300					305					310				
	Leu	Arg	Leu	Gly	Ser	Arg	Ala	Val	Phe	Ser	Thr	Thr	Asp	Glu	Glu	Gln
						320					325					330
	Ser	Ser	Ser	Ser	Val	Gly	Ser	Val	Ile	Asn	Ile	Asn	Asn	Leu	Ala	Ile
					335					340					345	
20	Asn	Leu	Pro	Ser	Ile	Leu	Gly	Asn	Arg	Val	Ala	Pro	Lys	Leu	Trp	Ile
			350						355					360		
	Arg	Pro	Thr	Gly	Ser	Ser	Ala	Pro	Tyr	Ser	Glu	Asp	Asn	Asn	Pro	Ile
			365					370					375			
	Ile	Asn	Leu	Ser	Gly	Pro	Leu	Ser	Leu	Leu	Asp	Asp	Glu	Asn	Leu	Asp
			380				385					390				
30	Pro	Tyr	Asp	Thr	Ala	Asp	Leu	Ala	Gln	Pro	Ile	Ala	Glu	Val	Pro	Leu
						400					405					410
	Leu	Tyr	Leu	Leu	Asp	Val	Thr	Ala	Lys	His	Ile	Asn	Thr	Asp	Asn	Phe
					415					420					425	
	Tyr	Pro	Glu	Gly	Leu	Asn	Thr	Thr	Gln	His	Tyr	Gly	Tyr	Gln	Gly	Val
				430					435					440		
40	Trp	Ser	Pro	Tyr	Trp	Ile	Glu	Thr	Ile	Thr	Thr	Ser	Asp	Thr	Ser	Ser
			445					450					455			
	Glu	Asp	Thr	Val	Asn	Thr	Leu	His	Arg	Gln	Leu	Tyr	Gly	Asp	Trp	Thr
							465					470				
	Pro	Thr	Gly	Tyr	Lys	Val	Asn	Pro	Glu	Asn	Lys	Gly	Asp	Ile	Ala	Leu
						480					485					490
	Ser	Ala	Phe	Trp	Gln	Ser	Phe	His	Asn	Leu	Phe	Ala	Thr	Leu	Arg	Tyr
					495					500					505	
50	Gln	Thr	Gln	Gln	Gly	Gln	Ile	Ala	Pro	Thr	Ala	Ser	Gly	Glu	Ala	Thr
					510				515					520		
	Arg	Leu	Phe	Val	His	Gln	Asn	Ser	Asn	Asn	Asp	Ala	Lys	Gly	Phe	His
					525			530					535			
	Met	Glu	Ala	Thr	Gly	Tyr	Ser	Leu	Gly	Thr	Thr	Ser	Asn	Thr	Ala	Ser
							545					550				
60	Asn	His	Ser	Phe	Gly	Val	Asn	Phe	Ser	Gln	Leu	Phe	Ser	Asn	Leu	Tyr
						560					565					570

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	Glu	Ser	His	Ser	Asp	Asn	Ser	Val	Ala	Ser	His	Thr	Thr	Thr	Val	Ala
					575					580					585	
	Leu	Gln	Ile	Asn	Pro	Trp	Leu	Gln	Glu	Arg	Phe	Ser	Thr	Ser	Ala	
				590				595					600			
10	Ser	Leu	Ala	Tyr	Ser	Tyr	Ser	Asn	His	His	Ile	Lys	Ala	Ser	Gly	Tyr
			605					610					615			
	Ser	Gly	Lys	Ile	Gln	Thr	Glu	Gly	Lys	Cys	Tyr	Ser	Thr	Thr	Leu	Gly
			620				625					630				
	Ala	Ala	Leu	Ser	Cys	Ser	Leu	Ser	Leu	Gln	Trp	Arg	Ser	Arg	Pro	Leu
						640					645				650	
	His	Phe	Thr	Pro	Phe	Ile	Gln	Ala	Ile	Ala	Val	Arg	Ser	Asn	Gln	Thr
					655					660					665	
20	Ala	Phe	Gln	Glu	Ser	Gly	Asp	Lys	Ala	Arg	Lys	Phe	Ser	Val	His	Lys
				670					675					680		
	Pro	Leu	Tyr	Asn	Leu	Thr	Val	Pro	Leu	Gly	Ile	Gln	Ser	Ala	Trp	Glu
								690					695			
	Ser	Lys	Phe	Arg	Leu	Pro	Thr	Tyr	Trp	Asn	Ile	Glu	Leu	Ala	Tyr	Gln
							705					710				
30	Pro	Val	Leu	Tyr	Gln	Gln	Asn	Pro	Glu	Ile	Asn	Val	Ser	Leu	Glu	Ser
						720					725				730	
	Ser	Gly	Ser	Ser	Trp	Leu	Leu	Ser	Gly	Thr	Thr	Leu	Ala	Arg	Asn	Ala
					735					740					745	
	Ile	Ala	Phe	Lys	Gly	Arg	Asn	Gln	Ile	Phe	Ile	Phe	Pro	Lys	Leu	Ser
					750				755					760		
40	Val	Phe	Leu	Asp	Tyr	Gln	Gly	Ser	Val	Ser	Ser	Ser	Thr	Thr	His	
								770					775			
	Tyr	Leu	His	Ala	Gly	Thr	Thr	Phe	Lys	Phe						
								785								
	<210> 42															
	<211> 1000															
	<212> PRT															
50	<213> Chlamydia pneumoniae															
	<400> 42															
	Met	Gln	Val	Phe	Pro	Lys	Val	Thr	Leu	Ser	Leu	Asp	Tyr	Ser	Ala	Asp
	1				5						10				15	
	Ile	Ser	Ser	Ser	Thr	Leu	Ser	His	Tyr	Leu	Asn	Val	Ala	Ser	Arg	Met
					20				25					30		
	Arg	Phe	Leu	Thr	Ile	Ser	Asp	Gln	Asn	Arg	Lys	Ile	Lys	Glu	Pro	Leu
					35			40					45			

72/83

Val Ser Lys Thr Pro Pro Lys Phe Leu Phe Tyr Leu Gly Asn Phe Thr  
 50 55 60  
 Ala Cys Met Phe Gly Met Thr Pro Ala Val Tyr Ser Leu Gln Thr Asp  
 65 70 75 80  
 10 Ser Leu Glu Lys Phe Ala Leu Glu Arg Asp Glu Glu Phe Arg Thr Ser  
 85 90 95  
 Phe Pro Leu Leu Asp Ser Leu Ser Thr Leu Thr Gly Phe Ser Pro Ile  
 100 105 110  
 Thr Thr Phe Val Gly Asn Arg His Asn Ser Ser Gln Asp Ile Val Leu  
 115 120 125  
 20 Ser Asn Tyr Lys Ser Ile Asp Asn Ile Leu Leu Leu Trp Thr Ser Ala  
 130 135 140  
 Gly Gly Ala Val Ser Cys Asn Asn Phe Leu Leu Ser Asn Val Glu Asp  
 145 150 155 160  
 His Ala Phe Phe Ser Lys Asn Leu Ala Ile Gly Thr Gly Gly Ala Ile  
 165 170 175  
 Ala Cys Gln Gly Ala Cys Thr Ile Thr Lys Asn Arg Gly Pro Leu Ile  
 180 185 190  
 30 Phe Phe Ser Asn Arg Gly Leu Asn Asn Ala Ser Thr Gly Gly Glu Thr  
 195 200 205  
 Arg Gly Gly Ala Ile Ala Cys Asn Gly Asp Phe Thr Ile Ser Gln Asn  
 210 215 220  
 Gln Gly Thr Phe Tyr Phe Val Asn Asn Ser Val Asn Asn Trp Gly Gly  
 225 230 235 240  
 40 Ala Leu Ser Thr Asn Gly His Cys Arg Ile Gln Ser Asn Arg Ala Pro  
 245 250 255  
 Leu Leu Phe Phe Asn Asn Thr Ala Pro Ser Gly Gly Gly Ala Leu Arg  
 260 265 270  
 Ser Glu Asn Thr Thr Ile Ser Asp Asn Thr Arg Pro Ile Tyr Phe Lys  
 275 280 285  
 Asn Asn Cys Gly Asn Asn Gly Gly Ala Ile Gln Thr Ser Val Thr Val  
 290 295 300  
 50 Ala Ile Lys Asn Asn Ser Gly Ser Val Ile Phe Asn Asn Asn Thr Ala  
 305 310 315 320  
 Leu Ser Gly Ser Ile Asn Ser Gly Asn Gly Ser Gly Gly Ala Ile Tyr  
 325 330 335  
 Thr Thr Asn Leu Ser Ile Asp Asp Asn Pro Gly Thr Ile Leu Phe Asn  
 340 345 350  
 60 Asn Asn Tyr Cys Ile Arg Asp Gly Gly Ala Ile Cys Thr Gln Phe Leu  
 355 360 365



73/83

Thr Ile Lys Asn Ser Gly His Val Tyr Phe Thr Asn Asn Gln Gly Asn  
 370 375 380  
 Trp Gly Gly Ala Leu Met Leu Leu Gln Asp Ser Thr Cys Leu Leu Phe  
 385 390 395 400  
 10 Ala Glu Gln Gly Asn Ile Ala Phe Gln Asn Asn Glu Val Phe Leu Thr  
 405 410 415  
 Thr Phe Gly Arg Tyr Asn Ala Ile His Cys Thr Pro Asn Ser Asn Leu  
 420 425 430  
 Gln Leu Gly Ala Asn Lys Gly Tyr Thr Thr Ala Phe Phe Asp Pro Ile  
 435 440 445  
 20 Glu His Gln His Pro Thr Thr Asn Pro Leu Ile Phe Asn Pro Asn Ala  
 450 455 460  
 Asn His Gln Gly Thr Ile Leu Phe Ser Ser Ala Tyr Ile Pro Glu Ala  
 465 470 475 480  
 Ser Asp Tyr Glu Asn Asn Phe Ile Ser Ser Ser Lys Asn Thr Ser Glu  
 485 490 495  
 Leu Arg Asn Gly Val Leu Ser Ile Glu Asp Arg Ala Gly Trp Gln Phe  
 500 505 510  
 30 Tyr Lys Phe Thr Gln Lys Gly Gly Ile Leu Lys Leu Gly His Ala Ala  
 515 520 525  
 Ser Ile Ala Thr Thr Ala Asn Ser Glu Thr Pro Ser Thr Ser Val Gly  
 530 535 540  
 Ser Gln Val Ile Ile Asn Asn Leu Ala Ile Asn Leu Pro Ser Ile Leu  
 545 550 555 560  
 40 Ala Lys Gly Lys Ala Pro Thr Leu Trp Ile Arg Pro Leu Gln Ser Ser  
 565 570 575  
 Ala Pro Phe Thr Glu Asp Asn Asn Pro Thr Ile Thr Leu Ser Gly Pro  
 580 585 590  
 Leu Thr Leu Leu Asn Glu Glu Asn Arg Asp Pro Tyr Asp Ser Ile Asp  
 595 600 605  
 Leu Ser Glu Pro Leu Gln Asn Ile His Leu Leu Ser Leu Ser Asp Val  
 610 615 620  
 50 Thr Ala Arg His Ile Asn Thr Asp Asn Phe His Pro Glu Ser Leu Asn  
 625 630 635 640  
 Ala Thr Glu His Tyr Gly Tyr Gln Gly Ile Trp Ser Pro Tyr Trp Val  
 645 650 655  
 Glu Thr Ile Thr Thr Thr Asn Asn Ala Ser Ile Glu Thr Ala Asn Thr  
 660 665 670  
 60 Leu Tyr Arg Ala Leu Tyr Ala Asn Trp Thr Pro Leu Gly Tyr Lys Val  
 675 680 685

74/83

	Asn	Pro	Glu	Tyr	Gln	Gly	Asp	Leu	Ala	Thr	Thr	Pro	Leu	Trp	Gln	Ser
	690						695					700				
	Phe	His	Thr	Met	Phe	Ser	Leu	Leu	Arg	Ser	Tyr	Asn	Arg	Thr	Gly	Asp
	705					710				715					720	
10	Ser	Asp	Ile	Glu	Arg	Pro	Phe	Leu	Glu	Ile	Gln	Gly	Ile	Ala	Asp	Gly
				725						730					735	
	Leu	Phe	Val	His	Gln	Asn	Ser	Ile	Pro	Gly	Ala	Pro	Gly	Phe	Arg	Ile
				740					745					750		
	Gln	Ser	Thr	Gly	Tyr	Ser	Leu	Gln	Ala	Ser	Ser	Glu	Thr	Ser	Leu	His
			755					760					765			
	Gln	Lys	Ile	Ser	Leu	Gly	Phe	Ala	Gln	Phe	Phe	Thr	Arg	Thr	Lys	Glu
			770				775					780				
20	Ile	Gly	Ser	Ser	Asn	Asn	Val	Ser	Ala	His	Asn	Thr	Val	Ser	Ser	Leu
	785				790						795					800
	Tyr	Val	Glu	Leu	Pro	Trp	Phe	Gln	Glu	Ala	Phe	Ala	Thr	Ser	His	Ser
					805					810					815	
	Leu	Ala	Tyr	Gly	Tyr	Gly	Asp	His	His	Leu	His	Ala	Tyr	Ile	Arg	His
				820				825						830		
30	Ile	Lys	Asn	Arg	Ala	Glu	Gly	Thr	Cys	Tyr	Ser	His	Thr	Leu	Ala	Ala
			835					840					845			
	Ala	Ile	Gly	Cys	Ser	Phe	Pro	Trp	Gln	Gln	Lys	Ser	Tyr	Leu	His	Leu
			850				855					860				
	Ser	Pro	Phe	Val	Gln	Ala	Ile	Ala	Ile	Arg	Ser	His	Gln	Thr	Ala	Phe
					870					875					880	
40	Glu	Glu	Ile	Gly	Asp	Asn	Pro	Arg	Lys	Phe	Val	Ser	Gln	Lys	Pro	Phe
				885						890					895	
	Tyr	Asn	Leu	Thr	Leu	Pro	Leu	Gly	Ile	Gln	Gly	Lys	Trp	Gln	Ser	Lys
				900					905					910		
	Phe	His	Val	Pro	Thr	Glu	Trp	Thr	Leu	Glu	Leu	Ser	Tyr	Gln	Pro	Val
			915					920					925			
	Leu	Tyr	Gln	Gln	Asn	Pro	Gln	Ile	Gly	Val	Thr	Leu	Leu	Ala	Ser	Gly
			930				935						940			
50	Gly	Ser	Trp	Asp	Ile	Leu	Gly	His	Asn	Tyr	Val	Arg	Asn	Ala	Leu	Gly
					950					955					960	
	Tyr	Lys	Val	His	Asn	Gln	Thr	Ala	Leu	Phe	Arg	Ser	Leu	Asp	Leu	Phe
				965						970					975	
	Leu	Asp	Tyr	Gln	Gly	Ser	Val	Ser	Ser	Ser	Thr	Ser	Thr	His	His	Leu
				980					985					990		
60	Gln	Ala	Gly	Ser	Thr	Leu	Lys	Phe								
			995					1000								

75/83

<210> 43  
 <211> 931  
 <212> PRT  
 <213> Chlamydia pneumoniae

&lt;400&gt; 43

10 Met Leu Leu Pro Phe Thr Val Leu Ala Asn Glu Gly Leu Gln Leu  
 1 5 10 15

Pro Leu Glu Thr Tyr Ile Thr Leu Ser Pro Glu Tyr Gln Ala Ala Pro  
 20 25 30

Gln Val Gly Phe Thr His Asn Gln Asn Gln Asp Leu Ala Ile Val Gly  
 35 40 45

Asn His Asn Asp Phe Ile Leu Asp Tyr Lys Tyr Tyr Arg Ser Asn Gly  
 50 55 60

20 Gly Ala Leu Thr Cys Lys Asn Leu Leu Ile Ser Glu Asn Ile Gly Asn  
 65 70 75 80

Val Phe Phe Glu Lys Asn Val Cys Pro Asn Ser Gly Gly Ala Ile Tyr  
 85 90 95

Ala Ala Gln Asn Cys Thr Ile Ser Lys Asn Gln Asn Tyr Ala Phe Thr  
 100 105 110

30 Thr Asn Leu Val Ser Asp Asn Pro Thr Ala Thr Ala Gly Ser Leu Leu  
 115 120 125

Gly Gly Ala Leu Phe Ala Ile Asn Cys Ser Ile Thr Asn Asn Leu Gly  
 130 135 140

Gln Gly Thr Phe Val Asp Asn Leu Ala Leu Asn Lys Gly Gly Ala Leu  
 145 150 155 160

40 Tyr Thr Glu Thr Asn Leu Ser Ile Lys Asp Asn Lys Gly Pro Ile Ile  
 165 170 175

Ile Lys Gln Asn Arg Ala Leu Asn Ser Asp Ser Leu Gly Gly Gly Ile  
 180 185 190

Tyr Ser Gly Asn Ser Leu Asn Ile Glu Gly Asn Ser Gly Ala Ile Gln  
 195 200 205

50 Ile Thr Ser Asn Ser Ser Gly Ser Gly Gly Gly Ile Phe Ser Thr Gln  
 210 215 220

Thr Leu Thr Ile Ser Ser Asn Lys Lys Leu Ile Glu Ile Ser Glu Asn  
 225 230 235 240

Ser Ala Phe Ala Asn Asn Tyr Gly Ser Asn Phe Asn Pro Gly Gly Gly  
 245 250 255

Gly Leu Thr Thr Thr Phe Cys Thr Ile Leu Asn Asn Arg Glu Gly Val  
 260 265 270

60 Leu Phe Asn Asn Asn Gln Ser Gln Ser Asn Gly Gly Ala Ile His Ala  
 275 280 285

76/83

Lys Ser Ile Ile Ile Lys Glu Asn Gly Pro Val Tyr Phe Leu Asn Asn  
 290 295 300  
 Thr Ala Thr Arg Gly Gly Ala Leu Leu Asn Leu Ser Ala Gly Ser Gly  
 305 310 315 320  
 10 Asn Gly Ser Phe Ile Leu Ser Ala Asp Asn Gly Asp Ile Ile Phe Asn  
 325 330 335  
 Asn Asn Thr Ala Ser Lys His Ala Leu Asn Pro Pro Tyr Arg Asn Ala  
 340 345 350  
 Ile His Ser Thr Pro Asn Met Asn Leu Gln Ile Gly Ala Arg Pro Gly  
 355 360 365  
 20 Tyr Arg Val Leu Phe Tyr Asp Pro Ile Glu His Glu Leu Pro Ser Ser  
 370 375 380  
 Phe Pro Ile Leu Phe Asn Phe Glu Thr Gly His Thr Gly Thr Val Leu  
 385 390 395 400  
 Phe Ser Gly Glu His Val His Gln Asn Phe Thr Asp Glu Met Asn Phe  
 405 410 415  
 Phe Ser Tyr Leu Arg Asn Thr Ser Glu Leu Arg Gln Gly Val Leu Ala  
 420 425 430  
 30 Val Glu Asp Gly Ala Gly Leu Ala Cys Tyr Lys Phe Phe Gln Arg Gly  
 435 440 445  
 Gly Thr Leu Leu Leu Gly Gln Gly Ala Val Ile Thr Thr Ala Gly Thr  
 450 455 460  
 Ile Pro Thr Pro Ser Ser Thr Pro Thr Thr Val Gly Ser Thr Ile Thr  
 465 470 475 480  
 40 Leu Asn His Ile Ala Ile Asp Leu Pro Ser Ile Leu Ser Phe Gln Ala  
 485 490 495  
 Gln Ala Pro Lys Ile Trp Ile Tyr Pro Thr Lys Thr Gly Ser Thr Tyr  
 500 505 510  
 Thr Glu Asp Ser Asn Pro Thr Ile Thr Ile Ser Gly Thr Leu Thr Leu  
 515 520 525  
 Arg Asn Ser Asn Asn Glu Asp Pro Tyr Asp Ser Leu Asp Leu Ser His  
 530 535 540  
 50 Ser Leu Glu Lys Val Pro Leu Leu Tyr Ile Val Asp Val Ala Ala Gln  
 545 550 555 560  
 Lys Ile Asn Ser Ser Gln Leu Asp Leu Ser Thr Leu Asn Ser Gly Glu  
 565 570 575  
 His Tyr Gly Tyr Gln Gly Ile Trp Ser Thr Tyr Trp Val Glu Thr Thr  
 580 585 590  
 60 Thr Ile Thr Asn Pro Thr Ser Leu Leu Gly Ala Asn Thr Lys His Lys  
 595 600 605

77/83

Leu Leu Tyr Ala Asn Trp Ser Pro Leu Gly Tyr Arg Pro His Pro Glu  
 610 615 620  
 Arg Arg Gly Glu Phe Ile Thr Asn Ala Leu Trp Gln Ser Ala Tyr Thr  
 625 630 635 640  
 10 Ala Leu Ala Gly Leu His Ser Leu Ser Ser Trp Asp Glu Glu Lys Gly  
 645 650 655  
 His Ala Ala Ser Leu Gln Gly Ile Gly Leu Leu Val His Gln Lys Asp  
 660 665 670  
 Lys Asn Gly Phe Lys Gly Phe Arg Ser His Met Thr Gly Tyr Ser Ala  
 675 680 685  
 Thr Thr Glu Ala Thr Ser Ser Gln Ser Pro Asn Phe Ser Leu Gly Phe  
 690 695 700  
 20 Ala Gln Phe Phe Ser Lys Ala Lys Glu His Glu Ser Gln Asn Ser Thr  
 705 710 715 720  
 Ser Ser His His Tyr Phe Ser Gly Met Cys Ile Ala Lys Tyr Ser Leu  
 725 730 735  
 Gln Arg Val Ile Arg Leu Ser Val Ser Leu Ala Tyr Met Phe Thr Ser  
 740 745 750  
 30 Glu His Thr His Thr Met Tyr Gln Gly Leu Leu Glu Gly Asn Ser Gln  
 755 760 765  
 Gly Ser Phe His Asn His Thr Leu Ala Gly Ala Leu Ser Cys Val Phe  
 770 775 780  
 Leu Pro Gln Pro His Gly Glu Ser Leu Gln Ile Tyr Pro Phe Ile Thr  
 785 790 795 800  
 40 Ala Leu Ala Ile Arg Gly Asn Leu Ala Ala Phe Gln Glu Ser Gly Asp  
 805 810 815  
 His Ala Arg Glu Phe Ser Leu His Arg Pro Leu Thr Asp Val Ser Leu  
 820 825 830  
 Pro Val Gly Ile Arg Ala Ser Trp Lys Asn His His Arg Val Pro Leu  
 835 840 845  
 Val Trp Leu Thr Glu Ile Ser Tyr Arg Ser Thr Leu Tyr Arg Gln Asp  
 850 855 860  
 50 Pro Glu Leu His Ser Lys Leu Leu Ile Ser Gln Gly Thr Trp Thr Thr  
 865 870 875 880  
 Gln Ala Thr Pro Val Thr Tyr Asn Ala Leu Gly Ile Lys Val Lys Asn  
 885 890 895  
 Thr Met Gln Val Phe Pro Lys Val Thr Leu Ser Leu Asp Tyr Ser Ala  
 900 905 910  
 60 Asp Ile Ser Ser Ser Thr Leu Ser His Tyr Leu Asn Val Ala Ser Arg  
 915 920 925

78/83

Met Arg Phe  
930

<210> 44  
<211> 978  
<212> PRT  
<213> Chlamydia pneumoniae

10

<400> 44  
Met Pro Leu Ser Phe Lys Ser Ser Ser Phe Cys Leu Leu Ala Cys Leu  
1 5 10 15  
Cys Ser Ala Ser Cys Ala Phe Ala Glu Thr Arg Leu Gly Gly Asn Phe  
20 25 30

20

Val Pro Pro Ile Thr Asn Gln Gly Glu Glu Ile Leu Leu Thr Ser Asp  
35 40 45  
Phe Val Cys Ser Asn Phe Leu Gly Ala Ser Phe Ser Ser Phe Ile  
50 55 60

30

Asn Ser Ser Ser Asn Leu Ser Leu Leu Gly Lys Gly Leu Ser Leu Thr  
65 70 75 80  
Phe Thr Ser Cys Gln Ala Pro Thr Asn Ser Asn Tyr Ala Leu Leu Ser  
85 90 95  
Ala Ala Glu Thr Leu Thr Phe Lys Asn Phe Ser Ser Ile Asn Phe Thr  
100 105 110

Gly Asn Gln Ser Thr Gly Leu Gly Gly Leu Ile Tyr Gly Lys Asp Ile  
115 120 125  
Val Phe Gln Ser Ile Lys Asp Leu Ile Phe Thr Thr Asn Arg Val Ala  
130 135 140

40

Tyr Ser Pro Ala Ser Val Thr Thr Ser Ala Thr Pro Ala Ile Thr Thr  
145 150 155 160  
Val Thr Thr Gly Ala Ser Ala Leu Gln Pro Thr Asp Ser Leu Thr Val  
165 170 175  
Glu Asn Ile Ser Gln Ser Ile Lys Phe Phe Gly Asn Leu Ala Asn Phe  
180 185 190

50

Gly Ser Ala Ile Ser Ser Ser Pro Thr Ala Val Val Lys Phe Ile Asn  
195 200 205  
Asn Thr Ala Thr Met Ser Phe Ser His Asn Phe Thr Ser Ser Gly Gly  
210 215 220  
Gly Val Ile Tyr Gly Gly Ser Ser Leu Leu Phe Glu Asn Asn Ser Gly  
225 230 235 240  
Cys Ile Ile Phe Thr Ala Asn Ser Cys Val Asn Ser Leu Lys Gly Val  
245 250 255

60

79/83

Thr Pro Ser Ser Gly Thr Tyr Ala Leu Gly Ser Gly Gly Ala Ile Cys  
 260 265 270  
 Ile Pro Thr Gly Thr Phe Glu Leu Lys Asn Asn Gln Gly Lys Cys Thr  
 275 280 285  
 10 Phe Ser Tyr Asn Gly Thr Pro Asn Asp Ala Gly Ala Ile Tyr Ala Glu  
 290 295 300  
 Thr Cys Asn Ile Val Gly Asn Gln Gly Ala Leu Leu Leu Asp Ser Asn  
 305 310 315 320  
 Thr Ala Ala Arg Asn Gly Gly Ala Ile Cys Ala Lys Val Leu Asn Ile  
 325 330 335  
 20 Gln Gly Arg Gly Pro Ile Glu Phe Ser Arg Asn Arg Ala Glu Lys Gly  
 340 345 350  
 Gly Ala Ile Phe Ile Gly Pro Ser Val Gly Asp Pro Ala Lys Gln Thr  
 355 360 365  
 Ser Thr Leu Thr Ile Leu Ala Ser Glu Gly Asp Ile Ala Phe Gln Gly  
 370 375 380  
 Asn Met Leu Asn Thr Lys Pro Gly Ile Arg Asn Ala Ile Thr Val Glu  
 385 390 395 400  
 30 Ala Gly Gly Glu Ile Val Ser Leu Ser Ala Gln Gly Gly Ser Arg Leu  
 405 410 415  
 Val Phe Tyr Asp Pro Ile Thr His Ser Leu Pro Thr Thr Ser Pro Ser  
 420 425 430  
 Asn Lys Asp Ile Thr Ile Asn Ala Asn Gly Ala Ser Gly Ser Val Val  
 435 440 445  
 40 Phe Thr Ser Lys Gly Leu Ser Ser Thr Glu Leu Leu Pro Ala Asn  
 450 455 460  
 Thr Thr Thr Ile Leu Leu Gly Thr Val Lys Ile Ala Ser Gly Glu Leu  
 465 470 475 480  
 Lys Ile Thr Asp Asn Ala Val Val Asn Val Ala Gly Phe Ala Thr Gln  
 485 490 495  
 50 Gly Ser Gly Gln Leu Thr Leu Gly Ser Gly Gly Thr Leu Gly Leu Ala  
 500 505 510  
 Thr Pro Thr Gly Ala Pro Ala Ala Val Asp Phe Thr Ile Gly Lys Leu  
 515 520 525  
 Ala Phe Asp Pro Phe Ser Phe Leu Lys Arg Asp Phe Val Ser Ala Ser  
 530 535 540  
 Val Asn Ala Gly Thr Lys Asn Val Thr Leu Thr Gly Ala Leu Val Leu  
 545 550 555 560  
 60 Asp Glu His Asp Val Thr Asp Leu Tyr Asp Met Val Ser Leu Gln Ser  
 565 570 575

80/83

Pro Val Ala Ile Pro Ile Ala Val Phe Lys Gly Ala Thr Val Thr Lys  
 580 585 590  
 Thr Gly Phe Pro Asp Gly Glu Ile Ala Thr Pro Ser His Tyr Gly Tyr  
 595 600 605  
 10 Gln Gly Lys Trp Ser Tyr Thr Trp Ser Arg Pro Leu Ile Pro Ala  
 610 615 620  
 Pro Asp Gly Gly Phe Pro Gly Gly Pro Ser Pro Ser Ala Asn Thr Leu  
 625 630 635 640  
 Tyr Ala Val Trp Asn Ser Asp Thr Leu Val Arg Ser Thr Tyr Ile Leu  
 645 650 655  
 20 Asp Pro Glu Arg Tyr Gly Glu Ile Val Ser Asn Ser Leu Trp Ile Ser  
 660 665 670  
 Phe Leu Gly Asn Gln Ala Phe Ser Asp Ile Leu Gln Asp Val Leu Leu  
 675 680 685  
 Ile Asp His Pro Gly Leu Ser Ile Thr Ala Lys Ala Leu Gly Ala Tyr  
 690 695 700  
 Val Glu His Thr Pro Arg Gln Gly His Glu Gly Phe Ser Gly Arg Tyr  
 705 710 715 720  
 30 Gly Gly Tyr Gln Ala Ala Leu Ser Met Asn Tyr Thr Asp His Thr Thr  
 725 730 735  
 Leu Gly Leu Ser Phe Gly Gln Leu Tyr Gly Lys Thr Asn Ala Asn Pro  
 740 745 750  
 Tyr Asp Ser Arg Cys Ser Glu Gln Met Tyr Leu Leu Ser Phe Phe Gly  
 755 760 765  
 40 Gln Phe Pro Ile Val Thr Gln Lys Ser Glu Ala Leu Ile Ser Trp Lys  
 770 775 780  
 Ala Ala Tyr Gly Tyr Ser Lys Asn His Leu Asn Thr Thr Tyr Leu Arg  
 785 790 795 800  
 Pro Asp Lys Ala Pro Lys Ser Gln Gly Gln Trp His Asn Asn Ser Tyr  
 805 810 815  
 Tyr Val Leu Ile Ser Ala Glu His Pro Phe Leu Asn Trp Cys Leu Leu  
 820 825 830  
 50 Thr Arg Pro Leu Ala Gln Ala Trp Asp Leu Ser Gly Phe Ile Ser Ala  
 835 840 845  
 Glu Phe Leu Gly Gly Trp Gln Ser Lys Phe Thr Glu Thr Gly Asp Leu  
 850 855 860  
 Gln Arg Ser Phe Ser Arg Gly Lys Gly Tyr Asn Val Ser Leu Pro Ile  
 865 870 875 880  
 60 Gly Cys Ser Ser Gln Trp Phe Thr Pro Phe Lys Lys Ala Pro Ser Thr  
 885 890 895



81/83

Leu Thr Ile Lys Leu Ala Tyr Lys Pro Asp Ile Tyr Arg Val Asn Pro  
 900 905 910  
 His Asn Ile Val Thr Val Val Ser Asn Gln Glu Ser Thr Ser Ile Ser  
 915 920 925  
 10 Gly Ala Asn Leu Arg Arg His Gly Leu Phe Val Gln Ile His Asp Val  
 930 935 940  
 Val Asp Leu Thr Glu Asp Thr Gln Ala Phe Leu Asn Tyr Thr Phe Asp  
 945 950 955 960  
 Gly Lys Asn Gly Phe Thr Asn His Arg Val Ser Thr Gly Leu Lys Ser  
 965 970 975  
 Thr Phe  
 20 <210> 45  
 <211> 813  
 <212> PRT  
 <213> Chlamydia pneumoniae  
 <400> 45  
 Ser Ala Leu Gln Pro Thr Asp Ser Leu Thr Val  
 1 5 10  
 30 Glu Asn Ile Ser Gln Ser Ile Lys Phe Phe Gly Asn Leu Ala Asn Phe  
 15 20 25  
 Gly Ser Ala Ile Ser Ser Ser Pro Thr Ala Val Val Lys Phe Ile Asn  
 30 35 40  
 Asn Thr Ala Thr Met Ser Phe Ser His Asn Phe Thr Ser Ser Gly Gly  
 45 50 55  
 40 Gly Val Ile Tyr Gly Gly Ser Ser Leu Leu Phe Glu Asn Asn Ser Gly  
 60 65 70 75  
 Cys Ile Ile Phe Thr Ala Asn Ser Cys Val Asn Ser Leu Lys Gly Val  
 80 85 90  
 Thr Pro Ser Ser Gly Thr Tyr Ala Leu Gly Ser Gly Gly Ala Ile Cys  
 95 100 105  
 Ile Pro Thr Gly Thr Phe Glu Leu Lys Asn Asn Gln Gly Lys Cys Thr  
 110 115 120  
 50 Phe Ser Tyr Asn Gly Thr Pro Asn Asp Ala Gly Ala Ile Tyr Ala Glu  
 125 130 135  
 Thr Cys Asn Ile Val Gly Asn Gln Gly Ala Leu Leu Leu Asp Ser Asn  
 140 145 150 155  
 Thr Ala Ala Arg Asn Gly Gly Ala Ile Cys Ala Lys Val Leu Asn Ile  
 160 165 170  
 60 Gln Gly Arg Gly Pro Ile Glu Phe Ser Arg Asn Arg Ala Glu Lys Gly  
 175 180 185

82/83

Gly Ala Ile Phe Ile Gly Pro Ser Val Gly Asp Pro Ala Lys Gln Thr  
 190 195 200  
 Ser Thr Leu Thr Ile Leu Ala Ser Glu Gly Asp Ile Ala Phe Gln Gly  
 205 210 215  
 10 Asn Met Leu Asn Thr Lys Pro Gly Ile Arg Asn Ala Ile Thr Val Glu  
 220 225 230 235  
 Ala Gly Gly Glu Ile Val Ser Leu Ser Ala Gln Gly Gly Ser Arg Leu  
 240 245 250  
 Val Phe Tyr Asp Pro Ile Thr His Ser Leu Pro Thr Thr Ser Pro Ser  
 255 260 265  
 20 Asn Lys Asp Ile Thr Ile Asn Ala Asn Gly Ala Ser Gly Ser Val Val  
 270 275 280  
 Phe Thr Ser Lys Gly Leu Ser Ser Thr Glu Leu Leu Leu Pro Ala Asn  
 285 290 295  
 Thr Thr Thr Ile Leu Leu Gly Thr Val Lys Ile Ala Ser Gly Glu Leu  
 300 305 310 315  
 Lys Ile Thr Asp Asn Ala Val Val Asn Val Ala Gly Phe Ala Thr Gln  
 320 325 330  
 30 Gly Ser Gly Gln Leu Thr Leu Gly Ser Gly Gly Thr Leu Gly Leu Ala  
 335 340 345  
 Thr Pro Thr Gly Ala Pro Ala Ala Val Asp Phe Thr Ile Gly Lys Leu  
 350 355 360  
 Ala Phe Asp Pro Phe Ser Phe Leu Lys Arg Asp Phe Val Ser Ala Ser  
 365 370 375  
 40 Val Asn Ala Gly Thr Lys Asn Val Thr Leu Thr Gly Ala Leu Val Leu  
 380 385 390 395  
 Asp Glu His Asp Val Thr Asp Leu Tyr Asp Met Val Ser Leu Gln Ser  
 400 405 410  
 Pro Val Ala Ile Pro Ile Ala Val Phe Lys Gly Ala Thr Val Thr Lys  
 445 420 425  
 Thr Gly Phe Pro Asp Gly Glu Ile Ala Thr Pro Ser His Tyr Gly Tyr  
 430 435 440  
 50 Gln Gly Lys Trp Ser Tyr Thr Trp Ser Arg Pro Leu Leu Ile Pro Ala  
 445 450 455  
 Pro Asp Gly Gly Phe Pro Gly Gly Pro Ser Pro Ser Ala Asn Thr Leu  
 460 465 470 475  
 Tyr Ala Val Trp Asn Ser Asp Thr Leu Val Arg Ser Thr Tyr Ile Leu  
 480 485 490  
 60 Asp Pro Glu Arg Tyr Gly Glu Ile Val Ser Asn Ser Leu Trp Ile Ser  
 495 500 505

83/83

Phe Leu Gly Asn Gln Ala Phe Ser Asp Ile Leu Gln Asp Val Leu Leu  
                   510                  515                  520  
 Ile Asp His Pro Gly Leu Ser Ile Thr Ala Lys Ala Leu Gly Ala Tyr  
                   525                  530                  535  
 10 Val Glu His Thr Pro Arg Gln Gly His Glu Gly Phe Ser Gly Arg Tyr  
       540                  545                  550                  555  
 Gly Gly Tyr Gln Ala Ala Leu Ser Met Asn Tyr Thr Asp His Thr Thr  
                   560                  565                  570  
 Leu Gly Leu Ser Phe Gly Gln Leu Tyr Gly Lys Thr Asn Ala Asn Pro  
                   575                  580                  585  
 Tyr Asp Ser Arg Cys Ser Glu Gln Met Tyr Leu Leu Ser Phe Phe Gly  
                   590                  595                  600  
 20 Gln Phe Pro Ile Val Thr Gln Lys Ser Glu Ala Leu Ile Ser Trp Lys  
       605                  610                  615  
 Ala Ala Tyr Gly Tyr Ser Lys Asn His Leu Asn Thr Thr Tyr Leu Arg  
       620                  625                  630                  635  
 Pro Asp Lys Ala Pro Lys Ser Gln Gly Gln Trp His Asn Asn Ser Tyr  
                   640                  645                  650  
 30 Tyr Val Leu Ile Ser Ala Glu His Pro Phe Leu Asn Trp Cys Leu Leu  
       655                  660                  665  
 Thr Arg Pro Leu Ala Gln Ala Trp Asp Leu Ser Gly Phe Ile Ser Ala  
                   670                  675                  680  
 Glu Phe Leu Gly Gly Trp Gln Ser Lys Phe Thr Glu Thr Gly Asp Leu  
       685                  690                  695  
 40 Gln Arg Ser Phe Ser Arg Gly Lys Gly Tyr Asn Val Ser Leu Pro Ile  
       700                  705                  710                  715  
 Gly Cys Ser Ser Gln Trp Phe Thr Pro Phe Lys Lys Ala Pro Ser Thr  
                   720                  725                  730  
 Leu Thr Ile Lys Leu Ala Tyr Lys Pro Asp Ile Tyr Arg Val Asn Pro  
                   735                  740                  745  
 His Asn Ile Val Thr Val Val Ser Asn Gln Glu Ser Thr Ser Ile Ser  
                   750                  755                  760  
 50 Gly Ala Asn Leu Arg Arg His Gly Leu Phe Val Gln Ile His Asp Val  
       765                  770                  775  
 Val Asp Leu Thr Glu Asp Thr Gln Ala Phe Leu Asn Tyr Thr Phe Asp  
       780                  785                  790                  795  
 Gly Lys Asn Gly Phe Thr Asn His Arg Val Ser Thr Gly Leu Lys Ser  
                   800                  805                  810  
 60 Thr Phe